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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE
EXPRESSION IN HUMAN BREAST AND HBL 100 CELLS

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene
expression in a sample derived from human HBL 100 cells is described. Also described are single exon nucleic acid probes expressed
in the HBL 100 cells and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BREAST AND HBL 100
CELLS

5 CROSS REFERENCE TO RELATED APPLICATIONS

The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
10 benefit under 35 U.S.C. s 119(e) of U.S. provisional patent
application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456, :
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
15 UK patent application no. 0024263.6, filed October 4, 2000,
the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY

20 REFERENCE THEREOF

The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
25 triplicate, containing a file named pto_HBL100.txt, created
24 January 2001, having 11,029,597 bytes. The Sequence
Listing contained in said file on said disc is incorporated
herein by reference in its entirety.

30 Field of the Invention

The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
35 particular, the present invention relates to unique genome-

derived single exon nucleic acid probes expressed in human HBL 100 cells and single exon nucleic acid microarrays that include such probes.

5 Background of the Invention

For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4
10 (1973), these techniques were used principally as tools to further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had
15 been both informed and directed by that antecedent biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane
20 association, and by the predicted assembly of its gene via T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

25 More recently, however, the development of high throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes
30 understanding of the basic biology of the encoded protein product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of
35 mRNA - are of greatest initial interest. This "expressed

sequence tag" ("EST") approach has already yielded vast amounts of sequence data (see for example Adams et al., *Science* 252:1651 (1991); Williamson, *Drug Discov. Today* 4:115 (1999)). For nucleic acids sequenced by this approach, often the only biological information that is known *a priori* with any certainty is the likelihood of biologic expression itself. By virtue of the species and tissue from which the mRNA had originally been obtained, most such sequences are also annotated with the identity of the species and at least one tissue in which expression appears likely.

More recently, the pace of genomic sequencing has accelerated dramatically. When genomic DNA serves as the initial substrate for sequencing efforts, expression cannot be presumed; often the only *a priori* biological information about the sequence includes the species and chromosome (and perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence accumulation by directed, EST, and genomic sequencing approaches — and in particular, with the accumulation of sequence information from multiple genera, from multiple species within genera, and from multiple individuals within a species — there is an increasing need for methods that rapidly and effectively permit the functions of nucleic sequences to be elucidated. And as such functional information accumulates, there is a further need for methods of storing such functional information in meaningful and useful relationship to the sequence itself; that is, there is an increasing need for means and apparatus for annotating raw sequence data with known or predicted functional information.

Although the increase in the pace of genomic sequencing is due in large part to technological changes in sequencing strategies and instrumentation, Service, *Science* 280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),

there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears
5 the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found
10 by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST
15 sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of
20 the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and
25 most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function
30 difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al.,
35 *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et

al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,
Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol.*
Biol. 268:78-94 (1997), predict many putative genes without
known homology or function. Such programs are known,
5 however, to give high false positive rates. Burset et al.,
Genomics 34:353-367 (1996). Using a consensus obtained by
a plurality of such programs is known to increase the
reliability of calling exons from genomic sequence.
Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

10 Identification of functional genes from genomic
data remains, however, an imperfect art. For example, in
reporting the full sequence of human chromosome 21, the
Chromosome 21 Mapping and Sequencing Consortium reports
that prior bioinformatic estimates of human gene number may
15 need to be revised substantially downwards. *Nature*
405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus
that permit the functions of the regions identified
bioinformatically – and specifically, that permit the
20 expression of regions predicted to encode protein – readily
to be confirmed experimentally.

Recently, the development of nucleic acid
microarrays has made possible the automated and highly
parallel measurement of gene expression. Reviewed in
25 Schena (ed.), DNA Microarrays : A Practical Approach
(Practical Approach Series), Oxford University Press (1999)
(ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60
(1999); Schena (ed.), Microarray Biochip: Tools and
Technology, Eaton Publishing Company/BioTechniques Books
30 Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from
cDNA/EST libraries, either from those previously described
in the literature, such as those from the I.M.A.G.E.
consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or
35 from the construction of "problem specific" libraries

targeted at a particular biological question, R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the breast are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the breast, for the most part these disorders are believed to have polygenic etiologies. There is a need for methods and apparatus that permit prediction, diagnosis and prognosis of diseases of the human breast, particularly those diseases with polygenic etiology.

Summary of the Invention

The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present

invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

In particular, the invention provides novel
5 genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids
10 identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single
15 exon nucleic acid probes for measuring gene expression in a sample derived from human Breast, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 5,074 or a complementary sequence, or a portion of such a sequence.

20 By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably
25 amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality
30 of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000
35 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 10,058 or a complimentary sequence, or a
5 portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp,
10 preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least
15 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is
20 preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single
25 exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane
30 which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene,
35 polyacrylate, polymethylmethacrylate, polyvinylchloride,

polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of SEQ ID Nos. 5,075 - 10,058, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 5,074.

Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human Breast which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 5,074 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human Breast.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOS.: 5,075

- 10,058 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human Breast
5 which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 10,059 - 15,009 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human Breast.

10 Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15,
15 suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth
20 aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

25 Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or
30 fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3
35 and Cy5 although other suitable dyes will be known to those

skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human Breast, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human Breast; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the Breast of said eukaryote, said

probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

10 identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 10,058 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 5,075 - 10,058, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 -5,074.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 10,059 - 15,009.

35 Accordingly in a eleventh aspect of the invention

there is provided a peptide comprising a sequence as set out in any of SEQ ID NOs: 10,059 - 15,009, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

Detailed Description of the Invention

15 Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000);

in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

As used herein, the term "peptide" refers to a

sequence of amino acids. The sequences referred to as
PEPTIDE SEQ ID NOS.: are the predicted peptide sequences
that would be translated from one of the exons, or a
portion thereof set out in exon SEQ ID NOS.: The codons
5 encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined
nucleotide sequence or sequences can be and, preferably,
are fragments unique to that sequence or to one or a
combination of those sequences. A fragment unique to a
10 nucleic acid molecule is one that is a signature for the
larger nucleic acid molecule.

As used herein, the phrase "expression of a
probe" and its linguistic variants means that the ORF
present within the probe, or its complement, is present
15 within a target mRNA.

As used herein, "stringent conditions" refers to
parameters well known to those skilled in the art. When a
nucleic acid molecule is said to be hybridisable to another
of a given sequence under "stringent conditions" it is
20 meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding
pair" intends a pair of molecules that bind to one another
with high specificity. Binding pairs are said to exhibit
specific binding when they exhibit avidity of at least 10^7 ,
25 preferably at least 10^8 , more preferably at least 10^9
liters/mole. Nonlimiting examples of specific binding
pairs are: antibody and antigen; biotin and avidin; and
biotin and streptavidin.

As used herein with respect to the visual display
30 of annotated genomic sequence, the term "rectangle" means
any geometric shape that has at least a first and a second
border, wherein the first and second borders each are
capable of mapping uniquely to a point of another visual
object of the display.

35 As used herein, a "Mondrian" means a visual

display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

5

Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and
10 examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in
15 meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

20 FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length
25 shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color
30 hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

35 FIG. 7 is a pictorial representation of the

expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured
5 tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

10 FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a
15 BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases
20 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

25 Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad
30 outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original
35 sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor.. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI). Databases of genomic sequence from species other than

human, such as mouse, rat, *Arabidopsis*, *C. elegans*, *C. brigssii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

5 Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to,
10 encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing
15 somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which
20 relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

25 Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic
30 assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

35 The subset of sequences output from process 300

is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

5 Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by
10 incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for
15 incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process
20 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magneto-optical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output
25 from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational
30 substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process.
35 Often, data will be stored after each, or at least a

plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently
5 long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment
10 length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal
15 number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes
20 (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate
25 a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been
30 described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is
35 possible to query the database for newly added sequence,

either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic,
5 temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts
10 that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST
15 and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

20 If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the
25 database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to
30 report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional
35 preprocessing 24, suitable and specific for the desired

analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as
5 processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis.
10 Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

15 Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using
20 programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified
25 algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can
30 be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the
35 undesired sequence as, for example, by converting the

specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after

transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase
5 reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

10 Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to
15 process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report
20 consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7%
25 of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

30 Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process
35 can be repeated on the same input sequence, or subset

thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully

to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that
5 subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message,
10 reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

15 The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

20 As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The
25 combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In
30 particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

35 Putative ORFs as predicted by a consensus of gene

calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is
5 conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic)
10 sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500
15 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more
20 effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400
25 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs
30 predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at
35 amplifying pieces of such ORFs is low, and that such

putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been

obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology
5 : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory
10 Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material
15 flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the
20 absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial
25 advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support
30 substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

35 Typically, the support substrate will be glass,

although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, 5 polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even 10 spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

The amplified nucleic acids can be attached 15 covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

20 Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources 25 (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

As is well known in the art, microarrays 30 typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or 35 32 *E. coli* genes suffice to provide a robust measure of

background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural
5 nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the
10 immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates,
15 the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

20 For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using
25 nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid
30 probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For
35 example, each standard microscope slide can include at

least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

5 Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as
10 is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

 The genome-derived single exon microarrays
15 described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3)
20 those constructed from yeast genomic DNA.

 Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above,
25 it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question,
30 R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

 Such EST microarrays by definition can measure expression only of those genes found in EST libraries,
35 shown herein to represent only a fraction of expressed

genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message
5 successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression
10 measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences
15 that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription,
20 optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor
25 cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from
30 genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST
35 approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

5 As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a
10 spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

 In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention
15 lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T,
20 where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

 A further distinction, which also affects the specificity of hybridization, is occasioned by the typical
25 derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the
30 probes are amplified, rather than excised, from the vector.

 In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from
35 genomic DNA. Typically, therefore, at least about 50, 60,

70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage.

5 Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including
10 probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

15 As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes
20 disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific
25 primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the
30 genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even
35 smaller amount of nonspecific sequence that would

contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham *et al.*, *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the

probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the

present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

5 Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization
10 results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

 In contrast, the longer probe length of the
15 genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or
20 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

25 A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound
30 noncovalently to the substrate.

 Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large
35 percentage differences in the theoretically optimum

stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the
5 range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the
10 quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present
15 substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4
20 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons
25 on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm
30 expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50%
35 of protein-encoding genes have introns. In preferred

embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about
5 one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present
10 invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments,
15 through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA
20 sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single
25 cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased
30 commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a
35 fluorophore (fluorochrome; fluor; fluorescent dye); the

reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes
5 prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned
10 using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

15 Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for
20 subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for further use.

25 Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

30 In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher
35 density arrays, such as are provided by microtiter plates

having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-
5 noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each
10 probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3'
15 primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be
20 packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a
25 genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the
30 genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation
35 information, such as gene expression data. Such recordable

media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then
5 separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should
10 be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and
15 characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic
20 sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected
25 of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences,
30 SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query -
35 including information on identical sequences and

information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence - can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, 5 process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such 10 annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or 15 by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

20 The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the 25 information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively 30 described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an 35 annotated sequence, representation of individual

nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention
5 herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian
10 visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of
15 rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 - or through user intervention,
20 as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession
25 number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is
30 anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual
35 display 80 is used as a graphical user interface to

computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

5 Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle
10 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

 Where a single bioinformatic method or approach
15 identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of
20 horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

 Thus, rectangles 83a in FIG. 3 represent the
25 functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or
30 approach.

 Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from
35 GRAIL or GRAIL II, rectangles 83b can represent the results

from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions. However, the increased visual complexity occasioned by such

display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of

bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as

can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute

expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

30 Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present

invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of
5 single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present
10 invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example
15 readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 5,074 of these ORFs in HBL 100 cells.

20 The HBL 100 human breast cancer cell line was established in vitro from milk of an apparently healthy woman. The cells express a variant of SV40 large T antigen, and genomic DNA from HBL 100 cells possesses transforming activity associated with the viral
25 information. The HBL100 cell line is nontumorigenic, and acquires the capacity to invade normal tissues and to replace them by proliferation in vitro only at high passage levels (HPL); these epithelial cells are thus are a useful model for studying breast tumor progression in vitro. HBL
30 100 cells bind both epidermal growth factor (EGF) and glucocorticoids but are progesterone receptor negative.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in HBL 100 cells is currently available for use
35 in measuring the level of its ORF's expression in Breast.

Diseases of the breast are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the breast, for the most part these disorders are believed to have polygenic etiologies.

For example, according to the American Cancer Society (ACS), carcinoma of the breast is the second most common cancer in women and, after lung cancer, is the second deadliest. The ACS estimates that in the U.S. there occurred 182,800 new cases of malignant breast cancer in 2000, and about 40,800 deaths from the disease. Although incidence of breast cancer is said to have declined, the disease clearly continues to represent a serious risk to the health and life of American women. Indeed, about one in nine U.S. women will develop breast cancer in her lifetime, and at present mortality rates, about a third of such women will eventually die from the disease.

A variety of factors are known to increase the risk of breast carcinoma. Sex is one: breast cancer in men is rare. Age is another: as women age, their risk for developing breast cancer increases, a 70 year old woman having three times the risk of developing cancer and five times the risk of dying from the disease as compared to a 40 year old woman. Most breast cancers occur after age 50, although in women with a genetic susceptibility, breast cancer tends to occur at an earlier age than in sporadic cases. Reproductive and menstrual history are also known to affect risk, with risk increasing with early menarche and late menopause, and is reduced by early first full term pregnancy. Additional risk factors, oft-times termed "lifestyle factors", include weight gain, obesity, fat intake, alcohol consumption, and level of physical

activity.

That genetic factors underlie the etiology of breast cancer is suggested by the approximately two-fold increased risk for development of breast cancer by women with a first-degree relative who has also developed breast cancer. After gender and age, a positive family history is the strongest known predictive risk factor for breast cancer. Genetic linkage analysis in families with high rates of inherited cancer have facilitated the identification of several genes in which mutations can be shown to contribute substantially to the development and progression of breast cancer, including BRCA1, BRCA2, p53, and PTEN/MMAC1. Further study has made clear, however, that these genes are not alone sufficient to explain all genetic contributions to breast cancer.

For example, BRCA1 appears to be responsible for disease in up to 90% of families with both breast and ovarian cancer, but in only 45% of families with multiple cases of breast cancer without occurrence of ovarian cancer. And mutations in BRCA2, localized to the long arm of chromosome 13, are thought to account for only approximately 35% of multiple case breast cancer families. Furthermore, despite the strong correlation between germline mutations in BRCA1 or BRCA2 and development of breast cancer, only weak connections have been made between these genes and sporadic breast cancer.

Epistatic effects of BRCA1 and BRCA2 mutations on other genetic loci, only some of which have been identified, have been postulated to account for some of the deleterious effects of mutations in these two genes.

Thus, mutations in p53 seem to be much more frequent in BRCA1 breast cancers (20/26) and somewhat more frequent in BRCA2-associated breast cancers (10/22) than in grade-matched sporadic cancers (7/20). BRCA mutation-associated cancers contain p53 mutations not typically

found in sporadic breast cancer, and 12 individual
hereditary breast cancers have been shown to contain more
than a single p53 mutation. Mutations of BRCA1 and BRCA2
may thus confer a "mutator" phenotype permitting the
5 accumulation of genetic abnormalities, with p53
inactivation selected during tumor progression.

Additionally, genome-wide screening for
chromosomal gains or losses in breast cancers harboring
BRCA1 or BRCA2 mutations demonstrated more regions that
10 were amplified or deleted compared to controls, suggesting
a generalized increase in large-scale genomic instability.
Chromosomes 5q, 4q, and 4p had very frequent loss of
heterozygosity in BRCA1 tumors, while BRCA2 tumors were
characterized by losses at 13q (near the BRCA2 locus
15 itself) and 6q, and chromosomal gains at 17q (outside of
the HER2/neu locus) and 20q.

Mutations of other genes have also been
implicated in susceptibility to development or
aggressiveness of breast cancer. For example, germline
20 mutations in the ATM gene, localized to chromosome
11q22-23, result in an increased risk of breast cancer
among female heterozygote carriers with an estimated
relative risk of 3.9 to 6.4; it is unclear, however, if
mutations in the ATM gene itself contribute to breast
25 cancer.

Normal allelic variation in a variety of genes,
as opposed to frank mutation, may also influence
susceptibility to developing breast carcinoma and the
propensity for the disease to progress. Such
30 polymorphisms may thus explain why particular women or
ethnic groups who do not otherwise bear mutations in genes
known to be linked to breast cancer are at greater risk,
especially in the context of exposure to environmental
agents and other nonhereditary risk factors.
35 Polymorphically expressed genes may code for enzymes that

metabolize estrogens or detoxify drugs and environmental carcinogens.

For example, molecular epidemiologic studies of cancer of the breast have examined associations with p450 cytochrome genotypes including CYP1A1, CYP2D6, and CYP17. The CYP1A1 gene, located on chromosome 15q, encodes the enzyme aryl hydrocarbon hydroxylase (AHH), present in breast tissue, and which catabolizes polycyclic aromatic hydrocarbons and arylamines. AHH is strongly inducible, i.e., greater enzymatic activity is seen with greater exposure to substrates. AHH catalyzes the monooxygenation of polycyclic aromatic hydrocarbons to phenolic products and epoxides that may be carcinogenic. AHH is also involved in the conversion of estrogen to hydroxylated conjugated estrogens such as 2-hydroxyestradiol.

Three polymorphisms in the CYP1A1 gene have been identified: an MspI RFLP of the 3' end of the gene (MspI); an adenine to guanine mutation in exon 7, causing an isoleucine to valine substitution (Ile-Val); and a polymorphism of the CYP1A1 gene identified among Negroids. The frequencies of the MspI and Ile-Val polymorphisms vary considerably by race, being higher among Japanese and Hawaiian populations as compared with Caucasians and Negroids.

The CYP2D6 gene is located on chromosome 22q and encodes the enzyme debrisoquine hydroxylase, which metabolizes a variety of drugs and other xenobiotics. Like other polymorphically expressed p450 enzymes, it may activate procarcinogens or, conversely, detoxify carcinogens. A number of alleles have been characterized at the CYP2D6 locus. The "poor metabolizer" phenotype (CYP2D6 mutant/mutant genotype), which is rare in Asians, occurs in about 5% to 10% of Caucasians and in 2% of Negroids.

As another example, the N-acetyl transferase-1

(NAT1) and N-acetyl transferase-2 (NAT2) genes are located on chromosome 8q. Allelic variation in the NAT genes may contribute to variation in populations as to the susceptibility of individuals to development of breast carcinoma, particularly in the context of exposure to compounds present in tobacco. NAT2 detoxifies or, conversely, activates aromatic amines found in tobacco smoke such as 4-aminobiphenyl. Both phenotypic assays and genotypic assays for NAT2 can be used to classify individuals as rapid or slow acetylators. Genetic variants of the NAT2 gene have been cloned and 6 alleles at this locus have been identified: the F1 allele confers the fast acetylator phenotype. The distribution of NAT1 and NAT2 alleles differs widely between racial and ethnic groups.

As yet another example, the glutathione S-transferase-M1 (GSTM1) gene is located on chromosome 1 and the gene for glutathione S-transferase-T1 (GSTT1) is located on chromosome 11q. A glutathione S-transferase-P1 (GSTP1) gene has also been identified. Glutathione S-transferases detoxify a variety of carcinogens and cytotoxic drugs (for example, benzo(a)pyrene, monohalomethanes such as methyl chloride, ethylene oxide, pesticides, and solvents used in industry) by catalyzing the conjugation of a glutathione moiety to the substrate. Allelic variation in the glutathione-S-transferase genes may contribute to variation in populations as to the susceptibility of individuals to development of breast carcinoma, particularly in the context of exposure to environmental toxins. Individuals homozygous for deletions in the GSTM1, GSTT1, or GSTP1 genes may have a higher risk of cancer of the breast and other sites because of their impaired ability to metabolize and eliminate carcinogens.

GSTM1 is polymorphically expressed and 3 alleles at the GSTM1 locus have been identified: GSTM1-0

(homozygous deletion genotype), GSTM1a, and GSTM1b. The null allele (GSTM1-0) is present in about 38% to 67% of Caucasians and 22% to 35% of Negroids. GSTM is not expressed in breast tissue at high levels. Two functionally different genotypes at the GSTT1 locus have been described: GSTT1-0 (homozygous deletion genotype) and GSTT1-1 (genotypes with 1 or 2 undeleted alleles). A polymorphism of the GSTP1 gene, A313G (changing codon 105 from Ile to Val), has been identified. The GSTT1-0 allele has been associated with accelerated age of first breast cancer diagnosis as compared with the GSTT1-1 allele.

Many other genes have been suggested to be involved in the development and/or progression of breast cancer, either as a result of gain of function or loss of function mutations, or as a result of normal allelic variation within different populations. A nonexhaustive list of such genes, each followed by the gene's chromosomal location, if known, follows: AMPH 7p14-p13; AMPHL (BIN1, SH3P9) 2q14; API4 (survivin, SVV) 17q25(?); ARHA (ARH12, RhoA) 3p21.3; ARHC (RhoC) 1p21-p13; ATM (ATA, ATC) 11q22.3; BAG1 9p12; BARD1 2q34-q35; BCAR1 16q23.1; BCAR2; BCAR3 (NSP2); BCAS1 (NABC1, AIBC1) 20q13.2-q13.3; BRCA1 17q21; BRCA2 13q12.3; CCND1 (D11S287E, Cyclin D, PRAD1) 11q13; CD44 (MDU3, HA, MDU2) 11pter-p13; CD9 (p24, MIC3, BA2) 12p13; CDKN1B (KIP1, P27) 12p13; CDKN2A (P16, INK4A, MTS1) 9p21; COMT 22q11.2; COT (MAP3K8, TPL-2, EST) 10p11.2; CSK (c-src) 15q23-q25; CTSD (CPSD) 11p15.5; CYP17 10q24.3; CYP19 15q21.1; CYP1A1 (CYP1) 15q22-q24; CYP1B1 (GLC3A) 2p22-p21; EFNB2 (EPLG5, LERK5, ephrin-B2) 13q33; EIF3S6 (INT6) 8q22-q23; EIF4E (EIF-4E) 4q21-q25; EMS1 11q13; ERBB2 (HER2, NEU) 17q11.2-q12; ERBB3 (HER3) 12q13; ESR1 (ESRA) 6q25.1; ESR2 (ESRB, ERBeta) 14q; FGF8 (AIGF) 10q24; GSTM1 (GST1, MU) 1p13.3; GSTP1 (FAEES3, GST3, PI) 11q13; GSTT1 22q11.23; HRAS 11p15.5; HSPB1 (HSP27) 7q; HSPCA (HSP90A, HSPC1); HSPCB (HSP90B, HSPC2) 6p12; IGF1

12q22-q24.1; IGF1R (JTK13) 15q25-q26; IGF2
 11p15.5; IL6 (IFNB2) 7p21; ING1 13q34; KISS1 (KiSS-1) 1q32;
 KLK3 (PSA, APS) 19q13; LASP1 (MLN50) 17q11-q21.3; LIBC
 6q22; MAP2K4 (MKK4, SEK1, JNKK1) 17p11.2; MKI67 (Ki-67)
 5 10q25-qter; MMP11 (STMY3, STR3) 22q11.2; MMP2 (CLG4A, CLG4,
 GELA) 16q13; MUC1 (PUM, PEM) 1q21; MYC (CMYC, C-MYC)
 8q24.12-q24.13; NOTCH4 (INT3, NOTCH3) 6p21.3; PCNA 20p12;
 PI5 (maspin) 18q21.3; PLA1 (uPA, URK) 10q24; PSEN2
 (D21S21, HPS2, BCEI) 21q22.3; RARB (NR1B2, HAP) 3p24; RB1
 10 (Rb) 13q14.2; S100A4 (MTS1, P9KA, metastasin) 1q21;
 SLC22A1L (BWSCR1A, ORCTL2, IMPT1) 11p15.5; SNCG (BCSG1)
 10q23.2-q23.3; SRD5A2 2p23; STIP1 (HSP70) 11?; STK11 (LKB1,
 PJS) 19p13.3; TFAP2A (AP2, AP2TF) 6p24; TFAP2B (AP2B)
 6p12; TFAP2C 20q13.2; TFF1 (D21S21, BCEI) 21q22.3; TGFBR2
 15 3p22; TIMP2 17q25; TP53 (p53, P53) 17q13.1; TPD52 (D52)
 8q21; TPD52L1 (D53, hD53) 6q22-q23; TSG101 11p15.2-p15.1.

The etiology of non-cancerous disorders of the breast may also involve genetic factors. Such disorders include disorders of development, inflammatory diseases of
 20 the breast, fibrocystic changes, proliferative breast disease, and non-carcinoma tumors.

Disorders of development of the breast include supernumerary nipples or breasts; accessory axillary breast tissue; congenital inversion of the nipples; and
 25 macromastia.

Inflammatory diseases of the breast include acute mastitis; periductal mastitis, also called recurrent subareolar abscess and squamous metaplasia of the lactiferous ducts; mammary duct ectasia; fat necrosis; and
 30 granulomatous mastitis, including granulomatous lobular mastitis. Systemic granulomatous diseases that can affect the breast include Wegener granulomatosis and sarcoidosis.

Proliferative breast diseases include epithelial hyperplasia; sclerosing adenosis; and small duct
 35 papillomas. Non-carcinoma tumors include stromal tumors

including fibroadenoma and phyllodes tumor, and sarcomas that include angiosarcoma, rhabdomyosarcoma, liposarcoma, leiomyosarcoma, chondrosarcoma and osteosarcoma. Other breast tumors include epithelial cell tumors including
5 large duct papillomas.

The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human breast, particularly those
10 diseases with polygenic etiology. With each of the single exon probes described herein shown to be expressed at detectable levels in human breast cancer cells, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide
15 exceptionally high informational content for such studies.

For example, diagnosis, grading, and/or staging of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known to be characteristic of
20 a given breast disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the
25 patient's breast to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids from individuals with known disease. Methods for quantitatively relating gene expression profiles, without regard to the
30 function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be
35 used to interrogate genomic DNA, rather than pools of

expressed message; this latter approach permits predisposition to and/or prognosis of breast disease to be assessed through the massively parallel determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human breast. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art — see Ausubel et al. and Maniatis et al. — each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the HBL 100 cells has been demonstrated are useful for both measurement in the Breast and for survey of expression in other tissues.

Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or

tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

5 The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

10 Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

15 Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999);
25 Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

35 Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for

example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al.,
5 "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and
10 Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the
15 Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

20 In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change,
25 serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway
30 of which the gene's expressed protein is a part.

Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead compound derivatives - the inability of the agent to alter
35 a gene's expression level is evidence that the drug does

not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in HBL 100 cells. The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the

hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known amplification technique. One such technique additional to
5 PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are
10 to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form suitable for amplification, the quantity need not be
15 sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be
20 packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific
5' primers used for genomic amplification can have a first
25 common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe
30 composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the
35 present invention will typically average at least about

100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the
5 genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however - that is, for use in a hybridization reaction in which the probe is not first
10 bound to a support substrate (although the target may indeed be so bound) - length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that
15 dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human
20 genome. For hybridization to expressed message - a subset of target sequence that is much reduced in complexity as compared to genomic sequence - even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention
25 can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 5,075 - 10,058, respectively, for probe SEQ ID NOS. 1 - 5,074. The minimum amount of ORF required to be included in the probe of the present invention in order to
30 provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 5,075 - 10,058 individually by routine experimentation using standard high stringency conditions.

35 Such high stringency conditions are described,

inter alia, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_{ot}1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded

probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in
5 both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and
10 below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that
15 the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can
20 usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

Green and other labels described in Haugland,
25 *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for
30 ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be
35 provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human HBL 100 cells.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term

"microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human HBL 100 cells. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 5,074.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 5,074 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 5,075 - 10,058, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 5,074 can be used, or that portion thereof in SEQ ID NOS. 5,075 - 10,058

used, to express a protein domain by standard in vitro recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X[™] Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL[™]) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, inter alia, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 5,075 - 10,058. Such amino acid sequences are set out in SEQ ID NOS: 10,059 - 15,009. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted
5 in Human Genomic Sequence

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces
that had been accessioned in a five month period
10 immediately preceding this study were downloaded from
GenBank. This corresponds to ~2200 clones, totaling ~350
MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the
program CROSS_MATCH, the sequence was analyzed for open
15 reading frames using three separate gene finding programs.
The three programs predict genes using independent
algorithmic methods developed on independent training sets:
GRAIL uses a neural network, GENEFINDER uses a hidden
Markoff model, and DICTION, a program proprietary to
20 Genetics Institute, operates according to a different
heuristic. The results of all three programs were used to
create a prediction matrix across the segment of genomic
DNA.

The three gene finding programs yielded a range
25 of results. GRAIL identified the greatest percentage of
genomic sequence as putative coding region, 2% of the data
analyzed. GENEFINDER was second, calling 1%, and DICTION
yielded the least putative coding region, with 0.8% of
genomic sequence called as coding region.

30 The consensus data were as follows. GRAIL and
GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and
DICTION agreed on 0.5% of genomic sequence, and the three
programs together agreed on 0.25% of the data analyzed.
That is, 0.25% of the genomic sequence was identified by
35 all three of the programs as containing putative coding

region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

10

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant

further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon
5 to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR®
10 green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

15 The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue
20 (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR
25 amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR
30 failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene
35 finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular
5 Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence
10 or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent
15 empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was
20 observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using
25 commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of
30 background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified)
35 produced an exact match (BLAST Expect ("E") values less

than 1×10^{-100}) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from 1×10^{-5} to 1×10^{-99}). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., Nature Genet. 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

5

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

10

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding

35

1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

5 Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 µl hybridization solution containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2
10 µg/µl human c₀t1 DNA, and 0.5 % SDS.

 Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2%
15 SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

 Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray
20 Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

 Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it
25 attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter,
30 "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

 Data were accepted for further analysis only when signal was at least three times greater than biological
35 noise, the latter defined by the average signal produced by

the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

5 FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues
10 tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant
15 signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single
20 tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of
25 all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the
30 respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using
35 the probe sequence. The legend for "bioinformatic

expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity

for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray

experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray

hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normal ized Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding

				protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter

confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain

were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1 α (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai et al., *Genomics* 49(2):283-89 (1998))(AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature. (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 \pm 0.11	-1.85 \pm 0.08
Brain	-1.41 \pm 0.11	-1.17 \pm 0.05
BT474	1.85 \pm 0.09	1.66 \pm 0.12
Fetal Liver	-1.62 \pm 0.07	-1.41 \pm 0.05
HBL100	1.32 \pm 0.05	2.64 \pm 0.12

Heart	1.16 ± 0.09	1.56 ± 0.10
HeLa	1.11 ± 0.06	1.30 ± 0.15
Liver	-1.62 ± 0.22	$-2.07 \pm$
Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases

25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

5 As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION identified 7 of the known exons (19%).

10 Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

15 The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We
20 selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression
25 patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they
30 show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):
red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
35 turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S

ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

5 EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring
Human Gene Expression

The protocols set forth in Examples 1 and 2,
10 *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in HBL 100 cells.

These unique exons are within longer probe
15 sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-
20 incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented
25 fragments of each of the 5,074 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

The structures of the 5,074 unique single exon probes are clearly presented in the Sequence Listing as SEQ
30 ID Nos.: 1 - 5,074. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 5,075 - 10,058,
35 respectively. It will be noted that some amplicons have

more than one exon, some exons are contained in more than one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is

distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human HBL 100 cells and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human HBL 100 cells.

10 The sequence of each of the exon probes identified by SEQ ID NOS.: 5,075 - 10,058 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because
15 the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the
20 three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were
25 found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe:"EXON
30 SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe,
35 the accession number of the database sequence that yielded

the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.

5 corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS... The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn
10 from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts
15 with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging
20 ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried
25 databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences
30 (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity
35 to sequences known to be expressed is of course arbitrary:

in Example 2, *supra*, a BLAST E value of $1e-30$ was used as the boundary when only two classes were to be defined for analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ - which is probative evidence that the query sequence has previously been shown to be expressed - the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 5,074) and probe exon (SEQ ID NOs.: 5,075 - 10,058, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring
Expression of Genes in Human HBL 100 cells

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Table 4 (209 pages) presents expression, homology, and
functional information for the genome-derived single exon
probes that are expressed significantly in human HBL 100
cells, a hormone sensitive human breast cancer cell line.

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
447	5484	10501	4.37				
878	5896	10837	8.5				
1028	6038		2.62				
1283	6282	11324	8.84				
1577	6574	11636	3.1				
1596	6592	11653	4.71				
1687	6683	11758	2.18				
1710	6705	11781	1.16				
1717	6712	11789	7.06				
1850	6839	11928	1.12				
1933	6919	12018	1.75				
2101	7082	12197	1.88				
2216	7193	12315	4.79				
3112	8128	13148	3.32				
3366	8374	13394	1.09				
3437	8445	13471	12.48				
3481	8489		1.38				
3573	8580	13586	1.16				
3844	8846		1.1				
4074	9068	14058	1.73				
4139	9134	14117	6.13				
4211	9204		1.28				
4669	9874	14657	1.1				
4879	9858	14829	4.14				
4888	9867	14837	1.25				
2595	7558	12672	0.93	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2595	7558	12673	0.93	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2853	7873	12886	3.02	9.4E+00	AB043785.1	NT	Mus musculus AT3 gene for antithrombin, complete cds
437	5475	10491	2.23	8.4E+00	5031804	NT	Homo sapiens insulin receptor subunit 1 (IRS1) mRNA
2809	7928	12946	3.48	7.2E+00	L12051.1	NT	Lycopodium obscurum Mill. GTPase (SAR2) mRNA, complete cds
2809	7928	12947	3.48	7.2E+00	L12051.1	NT	Lycopodium obscurum Mill. GTPase (SAR2) mRNA, complete cds
3445	8453		0.71	5.8E+00	7661557	NT	Homo sapiens DESC1 protein (DESC1), mRNA

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4840	9625	14617	1.32	5.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
3949	8947		11.08	4.8E+00	AF185295.1	NT	Eunice australis histone H3 (H3) gene, partial cds
287	5345	10357	2.28	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA, clone IMAGE:4099716 5'
288	5345	10357	1.89	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA, clone IMAGE:4099716 5'
3200	8216	13237	1.53	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3469	8477		1.24	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
3424	8432	13458	4.3	3.9E+00	X64518.1	NT	N. tabacum chitinase gene 50 for class I chitinase C
4194	9187		0.7	3.9E+00	AF055486.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
2557	7522		1.46	3.8E+00	AE001582.1	NT	Helicobacter pylori, strain J99 section 123 of the complete genome
3912	8912	13907	11.92	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
5050	10021		1.5	3.7E+00	AF216280.1	NT	Mus musculus heterochromatin protein 1 alpha mRNA, complete cds
588	5619	10617	3.88	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSJUE10 5'
3174	8190	13211	0.95	3.5E+00	AF221538.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
1481	6478	11534	2.28	3.4E+00	AF254577.1	NT	Brassica napus RPB5d mRNA, complete cds
497	5533	10540	1.82	3.2E+00	X98422.1	NT	D. rerio zp-50 POU gene
4588	9578	14567	1.44	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
2764	7785	12808	2.05	3.0E+00	8923984	NT	Homo sapiens hypothetical protein PR00889 (PR00889), mRNA
1981	6947	12049	1.6	2.9E+00	AE002225.2	NT	Chlamydia pneumoniae AF39, section 53 of 94 of the complete genome
1430	6427	11485	4.89	2.8E+00	AF186398.1	NT	Buxus harlandii malate dehydrogenase K (malK) gene, partial cds; chloroplast gene for chloroplast product
1583	6589		1.65	2.8E+00	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
230	5293	10301	19.61	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phx3), mRNA
230	5293	10302	19.61	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phx3), mRNA
4538	9528	14514	5.78	2.6E+00	AF086749.1	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
1436	6433	11489	2.05	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
1436	6433	11490	2.05	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
2944	7963	12983	0.8	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
4752	9737	14723	5.52	2.4E+00	4503352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
1234	8232	11278	13.73	2.3E+00	Z46724.1	NT	G. domesticus artificial single chain antibody gene (L3)
4002	8998		1.54	2.3E+00	AJ401081.1	NT	Bos taurus partial cyb gene for cytochrome b
3910	8910	13906	1.11	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4186	9179	14162	4.09	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4186	9179	14163	4.09	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
584	7724	10597	7.72	2.1E+00	AF132612.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2948	7997	12985	1.2	2.1E+00	AF208532.1	NT	Homo sapiens fatty acid omega-hydroxylase CYP4A11 (CYP4A11) gene, complete cds
3507	8515		0.83	2.1E+00	AW449366.1	EST_HUMAN	U1-H-B13-aki-e-08-0-UI.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
1177	6179	11215	2.45	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1177	6179	11216	2.45	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1315	6312	11361	1.07	2.0E+00	AF204927.1	NT	Oryctolagus cuniculus Na ⁺ /K ⁺ -ATPase beta 1 subunit mRNA, complete cds
1540	6538		3.89	2.0E+00	P25582	SWISSPROT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2088	7069	12182	8.21	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
2088	7069	12183	8.21	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
3984	8982	13967	1.95	2.0E+00	AW664496.1	EST_HUMAN	h13c05.x1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
3984	8982	13968	1.95	2.0E+00	AW664496.1	EST_HUMAN	h13c05.x1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
3019	8036	13046	1.75	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3047	8064	13072	2.44	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (alpE) genes, complete cds
3047	8064	13073	2.44	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (alpE) genes, complete cds
1091	6098	11127	1.65	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2209	7188	12308	2.62	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2312	7287	12408	1.36	1.7E+00	A1141067.1	EST_HUMAN	oz43h05.x1 Soares_NhiHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
1993	6968	12074	8.04	1.6E+00	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
1992	6977	12081	2.96	1.6E+00	AF077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
1996	6880	12085	1.09	1.6E+00	Y11344.1	NT	Mus musculus ST6GaiNAcII gene, exon 2
2220	7197		4.52	1.6E+00	X98373.1	NT	B. nepus gene encoding endo-polygalacturonase
2891	7910	12931	1.57	1.6E+00	W58426.1	EST_HUMAN	zd2501.1 Soares_fetal_heart_NhiH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to gb:D29805 N-ACETYL LACTOSAMINE SYNTHASE (HUMAN);
3921	8921		5.49	1.6E+00	BF570077.1	EST_HUMAN	602180805T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
4226	9220	14198	1.68	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4226	9220	14200	1.68	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4911	9890	14863	2.77	1.6E+00	Y11344.1	NT	Mus musculus ST6GaiNAcII gene, exon 2
4911	9890	14864	2.77	1.6E+00	Y11344.1	NT	Mus musculus ST6GaiNAcII gene, exon 2
33	5113	10089	4.61	1.5E+00	U53449.1	NT	Rattus norvegicus Jun dimerization protein 2 (Jdp-2) mRNA, complete cds
231	5294	10303	1.98	1.5E+00	AE002201.2	NT	Chlamydomonas reinhardtii AR39, section 32 of 94 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
616	5843		1.7	1.5E+00	6752961	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metargidin) (Adam15), mRNA
2344	7318	12438	1.68	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2444	7414	12530	1.67	1.5E+00	6678350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3065	7318	12438	2.59	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
30	5110	10095	1.17	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
30	5110	10096	1.17	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
2272	7248		7.96	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds
2568	7560	12677	1.44	1.4E+00	X74463.1	NT	Human papillomavirus type 7, complete DNA
2701	7658	12771	3.21	1.4E+00	AF084564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2701	7658	12772	3.21	1.4E+00	AF084564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3259	8272		0.89	1.4E+00	5453733	NT	Homo sapiens Mad4 homolog (MAD4) mRNA
4453	9443		1.34	1.4E+00	BF691547.1	EST_HUMAN	602166687F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4287566 5'
4994	9966	14944	1.02	1.4E+00	BE972428.1	EST_HUMAN	601662250F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935556 5'
565	5598		1.44	1.3E+00	Z73640.1	NT	M.mucedo gene encoding 4-Dihydroxymethyl-trisporate dehydrogenase
891	5909	10949	2.13	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 25S rRNA gene, isolate Tibet
1112	6118		19.14	1.3E+00	Y19213.1	NT	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7
1278	6277	11318	14.53	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) [ZNF157] mRNA
1278	6277	11319	14.53	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) [ZNF157] mRNA
1338	6336		1.06	1.3E+00	U61730.2	NT	Coix lacryma-jobi dihydrodipicolinate synthase (dapA) genes, complete cds
1574	6571		2.03	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 68 of 85 of the complete genome
2479	7448		1.67	1.3E+00	BE966735.2	EST_HUMAN	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'
3517	8525	13536					Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P56), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
642	5670	10674	0.68	1.3E+00	AF016494.1	NT	z122d08.s1 Soares fetal_liver_splice_INFLS S1 Homo sapiens cDNA clone IMAGE:431535 3'
813	5834	10867	0.86	1.2E+00	AA676246.1	EST_HUMAN	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-III)
813	5834	10868	0.86	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-III)
813	5834	10869	0.86	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-III)
867	5895		1.83	1.2E+00	8924234	NT	Homo sapiens hypobulbar protein PRO3077 (PRO3077), mRNA
1143	6147	11179	6.07	1.2E+00	AF080245.2	NT	Elaeis oleifera sesquiterpene synthase mRNA, complete cds
1186	6187	11224	1.7	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1186	6187	11225	1.7	1.2E+00	AJ26242.1	NT	pea seed-borne mosaic virus complete genome
1960	6946	12048	0.97	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3092	8108	13124	6.13	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3092	8108	13125	6.13	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3213	8228		3.29	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3277	8289	13314	0.73	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3630	8636	13641	8.37	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
3880	8881	13884	2.04	1.2E+00	BF373570.1	EST_HUMAN	MRO-FT0175-050900-203-g06_1 FT0175 Homo sapiens cDNA
4174	8289	13314	0.97	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4273	9266	14257	1.01	1.2E+00	6980951	NT	Rattus norvegicus Glycine receptor alpha 2 subunit (glycine receptor, neonatal) (Glr2), mRNA
4346	9337		2.1	1.2E+00	MB7060.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4392	9383	14365	0.99	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4429	9419	14405	1.92	1.2E+00	AF166495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4458	9446		5.44	1.2E+00	Y09200.1	NT	T. plannatum chloroplast rbcL gene, partial
461	5498	10509	1	1.1E+00	D66980.1	NT	Human mRNA for KIAA0227 gene, partial cds
1725	6720	11798	1.36	1.1E+00	AW895393.1	EST_HUMAN	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
3255	8268	13280	7.24	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3255	8268	13291	7.24	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3406	8415	13443	0.72	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3479	8487		2.43	1.1E+00	8922973	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
3499	8507	13522	0.93	1.1E+00	AB08360.1	EST_HUMAN	wf54h11.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to SW:P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1 ;
3636	8642	13647	1.32	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3636	8642	13648	1.32	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3840	8842	13649	0.95	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3913	8913	13908	0.88	1.1E+00	6755205	NT	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Pamb7), mRNA
4094	9089		8.1	1.1E+00	5835331	NT	R. unicornis complete mitochondrial genome
4834	9818	14786	4.26	1.1E+00	U18466.1	NT	African swine fever virus, complete genome
4899	9878	14847	1.11	1.1E+00	X78425.1	NT	E. faecalis pbp5 gene
5024	9995	14958	0.71	1.1E+00	P25398	SWISSPROT	TELLURITE RESISTANCE PROTEIN TEHA
5058	10028	14998	0.97	1.1E+00	AJ251835.1	NT	Mus musculus Kcnq1, Ltrpc5, Mash2, Tapa-1, Tssc4 and Tssc6 genes, alternative transcripts
98	5175		3.83	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
113	5185	10194	2.17	1.0E+00	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
415	5452		2.22	1.0E+00	AB021684.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA and 26S rRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
671	5604	10802	1.57	1.0E+00	AJ251660.1	NT	Girardia ligirina mRNA for homeodomain transcription factor (so gene)
669	5694	10703	9.1	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
670	5695		0.89	1.0E+00	AF125984.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1365	7746		3.02	1.0E+00	X80416.1	NT	V. carteri Algal-CAM mRNA
1719	6714	11791	1.39	1.0E+00	AB008531.1	NT	Plautia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2414	7385	12504	1.05	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2414	7385	12505	1.05	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2806	7826	12841	3.99	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2806	7826	12842	3.99	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2897	7818		0.98	1.0E+00	O14226	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN C6F12.08C IN CHROMOSOME 1
3128	8142	13163	0.82	1.0E+00	AA028453.1	EST_HUMAN	af28g08.s1 Soares_tetral_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to
3519	5175		0.92	1.0E+00	U23808.1	NT	WP:CA2D8.3 CE04204 :contains element MER22 MER22 repetitive element
3597	8604	13612	1.71	1.0E+00	AJ223816.1	NT	Xenopus laevis rhodopsin gene, complete cds
3956	8954	13943	1	1.0E+00	AF223391.1	NT	Agaricus bisporus mRNA for tyrosinase
4153	8148		1.07	1.0E+00	8922245	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4660	9645	14633	1.73	1.0E+00	AL163247.2	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
4751	9736		1.35	1.0E+00	U75741.1	NT	Homo sapiens chromosome 21 segment HS21C047
4859	9940		0.93	1.0E+00	D10852.1	NT	Taenia ovis 45W antigen (ToW4) gene, complete cds
4978	9954		1.12	1.0E+00	AF200817.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
5031	10002		1.36	1.0E+00	AJ245481.2	NT	Pilot whale morbillivirus phosphoprotein (P) gene, partial cds
2568	7529	12647	0.95	9.9E-01	AL163302.2	NT	Human immunodeficiency virus type 1 proviral complete genome, isolate 95ML84
3524	8531		0.82	9.9E-01	AF174585.1	NT	Homo sapiens chromosome 21 segment HS21C102
519	5554	10557	0.97	9.8E-01	P22567	SWISSPROT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
2728	7686		0.98	9.8E-01	AF174644.1	NT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
4315	9307	14291	0.68	9.6E-01	AF197925.1	NT	Xenopus laevis rec GTPase mRNA, complete cds
4315	9307	14292	0.68	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4336	9327	14312	1.34	9.6E-01	AW799874.1	EST_HUMAN	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
2404	7375	12485	1.44	9.5E-01	7705591	NT	PM2-UM0053-240300-005-112 UM0053 Homo sapiens cDNA
3694	8698	13699	2.08	9.5E-01	BE902340.1	EST_HUMAN	Homo sapiens CGI-125 protein (LOC51003), mRNA
							601875638F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3694	8698	13700	2.08	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3128	8144		3.87	9.4E-01	AF165990.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds
3146	8162		1.76	9.4E-01	AF080595.1	NT	Pimplinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
1694	6889		1.02	9.3E-01	AF242382.1	NT	Homo sapiens phytenoyl-CoA hydroxylase (PHYH) gene, exon 5
2562	7528	12844	2.29	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
3166	8182	13205	3.17	9.2E-01	BE022702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'
2065	7047		2.24	9.1E-01	8923058	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3132	8148	13198	0.83	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
3132	8148	13169	0.83	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
4254	8248	14232	1.01	9.0E-01	AF089810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
4411	9401	14366	2.16	8.8E-01	O26350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
462	5489	10510	1.83	8.7E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2804	7824	12839	5.88	8.7E-01	AA595863.1	EST_HUMAN	nn05f11.s1 NCL CGAP_Pr4.1 Homo sapiens cDNA clone IMAGE:1076877
4847	9829		4	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put
471	6507		1.63	8.6E-01	X17012.1	NT	Rat IGFI gene for insulin-like growth factor II
848	5867	10908	8.21	8.6E-01	W69089.1	EST_HUMAN	zd44e03.r1 Soares fetal heart NBH19W Homo sapiens cDNA clone IMAGE:343516 5'
3539	8545	13552	0.72	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3710	8714	13716	1.03	8.6E-01	U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
732	5755	10776	2.07	8.3E-01	M93437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3021	8038	13047	3.04	8.3E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3905	8905	13903	2.61	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
1999	6982	12086	1.68	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2608	7570		1.22	8.2E-01	AW376990.1	EST_HUMAN	IL3-CT0219-161199-031-C08 CT0219 Homo sapiens cDNA
3819	8821	13828	0.93	8.2E-01	AF083417.1	NT	Tenaxylum orbiculare elongation factor 1-alpha mRNA, partial cds
4935	9912	14890	0.99	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2684	7642		0.93	8.1E-01	AF191839.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3376	8384	13404	2.84	8.1E-01	AF055066.1	NT	Homo sapiens MHC class 1 region
3376	8384	13405	2.84	8.1E-01	AF055066.1	NT	Homo sapiens MHC class 1 region
176	5240		2.17	8.0E-01	AJ271510.1	NT	Staphylococcus aureus partial pla gene for phosphatase acetyltransferase allele 15
286	5344	10356	8.83	8.0E-01	AJ132772.1	NT	Bos taurus full and rlf genes

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descripor
1884	6969		1.42	8.0E-01	BF530982.1	EST_HUMAN	602072473F1 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4215091 5'
3003	8021	13034	1.22	8.0E-01	AF127897.1	NT	Salnitri bollmensis olfactory receptor (SBO27) gene, partial cds
3239	8252	13273	1.18	8.0E-01	AB006193.1	NT	Mus musculus gene for ovalucal glycoprotein, complete cds
3621	8628		1.19	8.0E-01	AL162758.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 717
4402	9393	14377	7.03	8.0E-01	X83739.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
4822	9806	14788	1.12	8.0E-01	7657352	NT	Mus musculus myosin IXb (Myo9b), mRNA
451	5488	10503	1.55	7.9E-01	D11476.1	NT	Lymantria dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
705	5729		0.78	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1568	6565		14.05	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
2201	7179	12302	8.75	7.9E-01	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds
2202	7180	12303	1.53	7.9E-01	AF130459.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
3438	8446	13472	2.93	7.9E-01	AF228664.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4176	9170		0.79	7.9E-01	BE263812.1	EST_HUMAN	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4479	9469	14449	1.35	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
4479	9469	14460	1.35	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
865	5883		2.82	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2213	7190	12311	2.29	7.8E-01	AW959587.1	EST_HUMAN	EST371837 MAGE resequences, MAGF Homo sapiens cDNA
4563	9551	14537	0.79	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
4871	9850		1.51	7.8E-01	AW753363.1	EST_HUMAN	RC3-CT0254-130100-023-c02 CT0254 Homo sapiens cDNA
143	5209	10223	4.43	7.7E-01	AF184345.1	NT	Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
							Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Iaalpha) and major histocompatibility protein class II beta chain (Ib beta) genes, complete cds;
716	5739		1.61	7.7E-01	AF050157.1	NT	butyrophilin-like (NG9), butyrophilin-like
2640	7600	12714	1.56	7.7E-01	O33915	SWISSPROT	CITRATE SYNTHASE
3520	8527	13538	3.71	7.7E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4272	9265	14255	3.89	7.7E-01	AF199488.1	NT	Colurnix columbix japonica sub-species japonica beta-actin mRNA, partial cds
4272	9265	14256	3.89	7.7E-01	AF199488.1	NT	Colurnix columbix japonica sub-species japonica beta-actin mRNA, partial cds
509	5544		1.38	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
579	5611	10510	1	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT1) gene, exon 5
5070	10039	15006	0.95	7.5E-01	6981387	NT	Rattus norvegicus Protein phosphatase 1, catalytic subunit, beta isoform (Ppp1cb), mRNA
1113	8119	11147	1.25	7.4E-01	AI598146.1	EST_HUMAN	in14609.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167877 3' similar to contains Alu repetitive element; contains element MIR repetitive element :

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2281	7257	12375	0.97	7.4E-01	AB011105.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
3643	8649	13655	0.87	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
4184	9177	14161	8.61	7.4E-01	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C04c
5013	9984	14960	1.07	7.4E-01	AW270842.1	EST_HUMAN	xp83d04.x1 NCL_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2746951 3' similar to contains element
4483	9473	14453	0.84	7.3E-01	AE001169.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
4582	9550	14536	4.94	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5046	10017	14986	0.92	7.3E-01	AJ400891.1	NT	Clethrionomys glareolus partial mRNA for putative UDP-glycose
821	5841	12928.1	2.09	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
1917	6903	11997	3.43	7.2E-01	X79140.1	NT	N. labacum Nelf-4A13 mRNA
2392	7363	12485	1.25	7.2E-01	AB009605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
2993	8011	13023	1.4	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3370	8378	13398	2.78	7.2E-01	AF065606.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6(A-I) allele, complete cds
3533	8539	13545	0.98	7.2E-01	AB002307.1	NT	Human mRNA for KIAA0309 gene, partial cds
3780	8783	13787	2.44	7.2E-01	BF339350.1	EST_HUMAN	602036589F1 NCL_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4183222 5'
4624	9609	14597	3.41	7.2E-01	D90314.1	NT	L. mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
4949	9926	14904	1.37	7.2E-01	AF198779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2)
4949	9926	14905	1.37	7.2E-01	AF198779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2)
4975	9951	14929	0.78	7.2E-01	P33086	SWISSPROT	NUCLEOSIDE TRIPHOSPHATASE I (NUCLEOSIDE TRIPHOSPHATE PHOSPHOHYDROLASE I) (NPH I)
683	5707	10719	9.08	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform (RyR1), complete cds
2989	8007	13020	14.39	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4086	9080	14070	3.49	7.1E-01	7305360	NT	Mus musculus ologelin (Olog), mRNA
4086	9080	14071	3.49	7.1E-01	7305360	NT	Mus musculus ologelin (Olog), mRNA
1209	6209	11248	2.58	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1209	6209	11249	2.58	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2381	7353	12474	1.03	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Soares_multiple_sclerosis_2NbIMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2381	7353	12475	1.03	7.0E-01	N82412.1	EST_HUMAN	yz73e07.s1 Soares_multiple_sclerosis_2NbrHSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
4889	9868		1.81	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101;
955	5971	11004	15.93	6.9E-01	U69874.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
955	5971	11005	15.93	6.9E-01	U69874.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1291	6290	11334	1.72	6.9E-01	AA593530.1	EST_HUMAN	nm28e09.s1 NCI_CGAP_Gast1 Homo sapiens cDNA clone IMAGE:1085178 3'
3148	8164	13184	1.56	6.8E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
942	5959	10992	2.14	6.8E-01	AF017784.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2603	7565		1.2	6.8E-01	D90917.1	NT	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
4439	9429	14413	1.39	6.8E-01	J00762.1	NT	Rat(hooded) prolactin gene : exon III and flanks
286	5353	10366	24.4	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
337	5389	10398	21.87	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
2088	7067	12179	1.15	6.7E-01	AA451884.1	EST_HUMAN	zx12g12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element ;
2102	7763	12198	2.56	6.7E-01	AF188073.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
2927	7946	12963	4	6.7E-01	6678580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4331	9322	14308	0.7	6.7E-01	X74421.1	NT	S.tuberosum mRNA for glucose-6-phosphate dehydrogenase
2628	7588	12700	1.28	6.6E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3409	8418	13446	0.93	6.6E-01	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
3574	8581	13687	3.48	6.6E-01	Y07669.1	NT	C.albicans random DNA marker, 282bp
3993	8990		1.05	6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
618	5645	10847	1.67	6.5E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
618	5645	10848	1.67	6.5E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3348	8357	13375	4.84	6.5E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4159	9154	14137	5.18	6.5E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4894	9873	14840	2.32	6.5E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5073	10042	15008	1.39	6.5E-01	8924057	NT	Homo sapiens hypothetical protein PRO1580 (PRO1580), mRNA
250	6310	10321	8.85	6.4E-01	U48848.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
2511	7478	12594	0.9	6.4E-01	AF181184.1	NT	Pseudomonas fluorescens tryptophan halogenase (pinA) gene, complete cds
3374	8382	13402	3.74	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3771	8774	13778	1.19	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4364	9355	14334	0.74	6.4E-01	Y12488.1	NT	M.musculus whn gene
4364	9365	14335	0.74	6.4E-01	Y12488.1	NT	M.musculus whn gene
431	6469	10488	3.16	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONIE PFHRP-III)
531	5586	10569	1.73	6.3E-01	U32889.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2098	7078	12183	25.01	6.3E-01	U81136.1	NT	Shigella flexneri multi-antibiotic resistance locus
2503	7471	12587	1.82	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2503	7471	12588	1.82	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2949	7888		0.87	6.3E-01	Y17275.1	NT	Lycopodium obscurum p69a gene, complete cds
2330	7304		3.53	6.1E-01	6878076	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
4405	9398	14379	0.98	6.1E-01	4557538	NT	Homo sapiens solute carrier family 26 (sulfate transporter), member 2 (SLC26A2) mRNA
491	5527	10535	1.08	6.0E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
557	5591		2.78	6.0E-01	5802999	NT	Homo sapiens adaptor-related protein complex 3, mu2 subunit (CLA20), mRNA
1345	6342	11393	1.38	6.0E-01	AF085253.1	NT	Human respiratory syncytial virus strain CH93-53b attachment protein (G) gene, complete cds
3725	8729	13727	0.81	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
3923	8923	13914	2.18	6.0E-01	X16842.1	NT	Xenopus mRNA for desmin
4064	9058		1.03	6.0E-01	AF058895.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
985	6000	11031	1.03	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3186	8212	13233	9.18	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3186	8212	13234	9.18	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4100	9094		3	5.9E-01	AF162756.1	NT	Rattus norvegicus ceneidin 2 mRNA, partial cds
1866	6855	11943	1.05	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN
3876	8877	13980	0.97	5.8E-01	BF695736.1	EST_HUMAN	601852474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076131 5'
4383	9374	14353	4.1	5.8E-01	AB009077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
4652	9637		1.31	5.8E-01	AF110846.1	NT	Megascalis scalaris sex-lethal homolog (Megsxl) gene, partial cds, alternatively spliced products
4775	9759		2.28	5.8E-01	AW769483.1	EST_HUMAN	h164f10.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3005995 3'
1463	6460	11518	1.04	5.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
1463	6460	11519	1.04	5.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3152	8166	13188	1.38	5.7E-01	Q9WJT2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVO1A)
3425	8433		2.37	5.7E-01	AB033503.1	NT	Populus euramericana peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
5042	10013	14982	0.95	5.7E-01	L41867.1	NT	Drosophila extra sex combs gene, exon 1-4, complete cds
3283	8295	13320	1.11	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3283	8295	13321	1.11	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
4117	9111	14095	2.28	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
1192	6193	11230	1.79	5.5E-01	8393912	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2629	7589	12701	2.21	5.5E-01	P03341	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2629	7589	12702	2.21	5.5E-01	P03341	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2848	7868	12884	0.79	5.5E-01	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
2892	8010		1.33	5.5E-01	H46219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:178268 3'
3163	8179	13201	3.6	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3608	8615	13624	1.37	5.5E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
4982	9957	14935	0.99	5.5E-01	U69097.1	NT	Bos taurus MHC class II beta-chain BoLA-DIB1 gene, partial cds
144	5210	10224	13.58	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 Interacting nuclear target (MINT) homolog (KIAA0929), mRNA
144	5210	10225	13.58	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 Interacting nuclear target (MINT) homolog (KIAA0929), mRNA
580	5612	10511	1.77	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
580	5612	10512	1.77	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
1252	6250	11291	2.4	5.4E-01	AW896087.1	EST_HUMAN	QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2048	7030		2.35	5.4E-01	AE002247.2	NT	Chlamydia pneumoniae AR39, section 74 of 94 of the complete genome
2193	7172	12293	1.53	5.4E-01	AJ276882.1	NT	Drosophila melanogaster mRNA for 15.15' beta carotene dioxygenase (beta-diox gene)
512	5547	10552	1.61	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes >
2710	7667	12779	10.07	5.3E-01	4508328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2710	7667	12780	10.07	5.3E-01	4508328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3169	8185	13206	3.87	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LSCCL) gene, complete cds

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Table 4
Single Exon Probes Expressed in HBL100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4090	8084		1.22	5.3E-01	U39887.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
806	5827	10857	12.62	5.2E-01	L20770.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1146	8150	11182	11.32	5.2E-01	Q8WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5)
1171	6174	11208	6.03	5.2E-01	AF224492.1	NT	(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1847	6836		4.17	5.2E-01	AL163285.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
2085	7066	12178	1.52	5.2E-01	AB018283.2	NT	Homo sapiens chromosome 21 segment HS21C085
3046	8063	13071	1.72	6.2E-01	U65942.1	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3321	8331		11.56	6.2E-01	AL116780.1	NT	Chlamydomonas abortus strain S26/3 POMP91A and POMP90A precursor, genes, complete cds
3360	8368	13387	2.52	5.2E-01	AA084165.1	EST_HUMAN	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3547	8554		0.79	5.2E-01	AF020288.1	NT	em77g05.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
4358	9349		1.46	5.2E-01	AF093796.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
4860	9937		1.01	5.2E-01	AL163281.2	NT	Avian infectious bronchitis virus isolate variant 2 S1 spike glycoprotein gene, partial cds
613	5640	10843	1.9	6.1E-01	M58509.1	NT	Homo sapiens chromosome 21 segment HS21C081
640	5668	10671	3.68	5.1E-01	AJ233944.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
640	5668	10672	3.68	6.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain Pl vt1) 16S rRNA gene
3863	8961	13951	4.37	6.1E-01	AB58495.1	EST_HUMAN	Polyangium vitellinum (strain Pl vt1) 16S rRNA gene
4062	9056	14043	2.47	5.1E-01	P66380	SWISSPROT	w39b12.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427263 3'
2076	7058	12167	1.03	5.0E-01	4885552	NT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
2076	7058	12168	1.03	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2083	7084	12174	1.06	5.0E-01	AF008210.1	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2083	7084	12174	1.06	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene?
2083	7084	12174	1.06	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene?
3740	8744	13744	1.11	5.0E-01	L38483.1	NT	Rattus norvegicus jagged protein mRNA, complete cds
3782	8785	13788	2.97	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
781	5802	10832	2.67	4.9E-01	BF571462.1	EST_HUMAN	602076648F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4243860 5'
1619	6616	11682	4.93	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1864	8853	11941	1.9	4.9E-01	U40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
3460	8468		1.14	4.8E-01	AA912842.1	EST_HUMAN	ci32e09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1625144 3'
3656	8664	13669	1.62	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3658	8694	13670	1.62	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
2799	7819	12838	4.48	4.5E-01	AA677086.1	EST_HUMAN	456d02.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3243	8266	13277	4.25	4.5E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
3293	8304	13328	1.39	4.5E-01	AF126378.1	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
3917	8917		1.06	4.5E-01	Q28247	SWISSPROT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4052	10058		5.38	4.5E-01	AW873495.1	EST_HUMAN	COLLAGEN ALPHA 5(V) CHAIN
4786	9770	14754	1.55	4.5E-01	BE963445.2	EST_HUMAN	nc80g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
1985	6970		2.19	4.4E-01	6680503	NT	601657226R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866023 3'
2325	7289	12420	4.73	4.4E-01	P49785	SWISSPROT	Mus musculus integral membrane-associated protein 1 (lmap1), mRNA
3241	8254	13275	1.19	4.4E-01	AF058780.1	NT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3241	8254	13276	1.19	4.4E-01	AF058780.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3245	8258	13279	1.81	4.4E-01	BF056728.1	EST_HUMAN	Rattus norvegicus SynGAP-b mRNA, complete cds
4113	9107		1.55	4.4E-01	BE978707.1	EST_HUMAN	791d02.Y1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3393795 5'
4938	9915	14894	6.65	4.4E-01	U61154.1	NT	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609393 5'
408	5445	10465	1.95	4.3E-01	AF155218.1	NT	Buzura suppressaria nucleopolyhedrovirus ecdysteroid UDP-glucosyltransferase (egt) gene, complete cds
408	5445	10466	1.95	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
2801	7821		1.34	4.3E-01	AW835269.1	EST_HUMAN	Callithrix jacchus MW/LW opsin gene, upstream flanking region
2986	8004	13018	0.72	4.3E-01	AW899477.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
4028	8024	14011	1.2	4.3E-01	J00306.1	NT	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4282	5445	10465	1.07	4.3E-01	AF155218.1	NT	Human somatostatin 1 gene and flanks
4282	5445	10466	1.07	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4944	9921		1.08	4.3E-01	8635250	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
1341	7745	11389	1.24	4.2E-01	Q39102	SWISSPROT	Xestia c-higrum granulovirus, complete genome
3528	8534	13541	3.83	4.2E-01	AE003947.1	NT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
3552	8559	13565	2.9	4.2E-01	AI280338.1	EST_HUMAN	Xylella fastidiosa, section 93 of 229 of the complete genome
3629	10057		0.86	4.2E-01	N81203.1	EST_HUMAN	q194b01.x1 Soares_NhrHMPu_S1 Homo sapiens cDNA clone IMAGE:1879945 3'
4558	9546	14531	5.45	4.2E-01	AA534093.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40488
4636	9621	14613	3.8	4.2E-01	R13467.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS III HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
1077	6084	11113	1.52	4.1E-01	AI905481.1	EST_HUMAN	777601.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'
1086	6093	11122	2.09	4.1E-01	AV705243.1	EST_HUMAN	RC-BT091-210189-142 BT091 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1086	6093	11123	2.09	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1573	6570	11632	0.94	4.1E-01	AI905949.1	EST_HUMAN	PM-BT103-270499-684 BT103 Homo sapiens cDNA
2638	7598	12712	1.1	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2869	7888	12908	2.49	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2869	7888	12908	2.49	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3229	8244	13268	0.7	4.1E-01	AA906344.1	EST_HUMAN	q94b08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
4178	9147	14131	2.75	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 isoG, isoH, isoI, isoJ, isoK, isoL, isoM, isoN, isoO, isoP, isoQ, isoR, isoS, isoT, isoU, isoV, isoW, isoX, isoY, isoZ, isoAA, isoAB, isoAC, isoAD, isoAE and isoAF genes
4178	9147	14131	0.74	4.1E-01	AA909257.1	EST_HUMAN	cm33d02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'
4532	9522	14509	1.37	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
1022	6031	11061	0.81	4.0E-01	8404656	NT	Laqueus rubellus mitochondrion, complete genome
1318	6317	11365	1.16	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dmi) mRNA, complete cds
1454	6451	10222	3.09	4.0E-01	6679258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2733	5207	10222	2.12	4.0E-01	6678490	NT	Mus musculus ubiquitin-protein ligase e3 component n-1:ecognin (Ubr1), mRNA
2898	7017	12937	1.16	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2898	7017	12938	1.16	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3612	8619	13629	2.74	4.0E-01	AF068903.1	NT	Streptococcus pneumoniae Y1C (Y1C), Y1D (Y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3737	8741	13740	3.44	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3737	8741	13741	3.44	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4672	8657	11407	8.6	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
1359	6356	11407	1.57	3.9E-01	AF206618.1	NT	Gorilla gorilla carboxy-ester lipase (CEL) gene, complete cds
2571	7534	12651	2.87	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2633	7593	12705	2.98	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
2633	7593	12705	2.98	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
3023	8040	13049	4.17	3.9E-01	AJ225896.1	NT	Sinorhizobium meliloti egl, syB2, cya3 genes and orf3
3984	8962	13952	1.39	3.9E-01	BF592611.1	EST_HUMAN	761d01.x1 NCL_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3339169 3'
159	5225		27.46	3.8E-01	7019488	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
502	5537		3.87	3.8E-01	AB029291.1	NT	Mus musculus pcm-1 mRNA for pericentriolar material-1, complete cds
2486	7484	12579	3.42	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myb-like transcription factor (MYB3R-3) mRNA, complete cds
2560	7775	12841	3.09	3.8E-01	6678002	NT	Mus musculus solute carrier family 1, member 8 (Slc1a6), mRNA
2933	7962		0.82	3.8E-01	AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)
2974	7992	13007	2.37	3.8E-01	AF0439383.1	NT	Pleurococcus americanus aminopeptidase N (ampN) gene, partial cds
3403	8412	13438	8.3	3.8E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3461	8469		0.77	3.8E-01	AB07219.1	EST_HUMAN	w38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3671	8676	13679	0.93	3.8E-01	BE154080.1	EST_HUMAN	PMO-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
2410	7381	12489	5.9	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3378	8386	13407	10.03	3.7E-01	AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
3779	8782	13786	1.12	3.7E-01	AA319482.1	EST_HUMAN	EST21715 Adrenal gland tumor Homo sapiens cDNA 5' end
4108	9102	14089	7.57	3.7E-01	A218707.1	EST_HUMAN	ok39c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510188 3'
4193	9186	14167	1.55	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4265	9258	14248	3.38	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 208 of the complete genome
980	5995		8.26	3.6E-01	U89241.1	NT	Human mlbp gene, partial cds
1285	6293	11339	2.38	3.6E-01	T80255.1	EST_HUMAN	yd03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1295	6293	11340	2.38	3.6E-01	T80255.1	EST_HUMAN	yd03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1872	6881	11949	3.81	3.6E-01	AW590184.1	EST_HUMAN	hg33102.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1872	6881	11950	3.81	3.6E-01	AW590184.1	EST_HUMAN	hg33102.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1912	6898	11993	4.6	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2208	7185		0.97	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2326	7300		2.82	3.6E-01	X76725.1	NT	P Irregular (P3804) gene for actin
2417	7388	12508	0.95	3.6E-01	AW812033.1	EST_HUMAN	RC8-ST0171-181099-011-g07 ST0171 Homo sapiens cDNA
2558	7523	12639	1.1	3.6E-01	P24206	SWISSPROT	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2828	10055		7.88	3.6E-01	AF189485.1	NT	Drosophila melanogaster sugar transporter 3 (sut3) mRNA, complete cds
3388	8386	13420	1.83	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3388	8386	13421	1.83	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4284	9278	14284	0.98	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA
4810	9598	14582	1.49	3.6E-01	Y11526.1	NT	Z. mays mRNA for casein kinase II alpha subunit
4849	9831	14806	2.78	3.6E-01	AW339393.1	EST_HUMAN	ha02g04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'
5037	10008	14978	1.25	3.6E-01	AE001187.1	NT	Treponema pallidum section 3 of 87 of the complete genome
115	5187	10198	0.85	3.5E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
209	5273	10285	2.22	3.5E-01	6878933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
715	5738	10755	1.11	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
715	5738	10756	1.11	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
771	5793	10821	2.75	3.5E-01	BF129796.1	EST_HUMAN	601811050R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
1580	6577	11641	0.92	3.5E-01	BF310698.1	EST_HUMAN	601894653F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5'

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1600	6596	11657	2	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2219	7198	12318	1.43	3.5E-01	P08798	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3)
2531	7774	12616	1.81	3.5E-01	AA229252.1	EST_HUMAN	z08a09.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:850872 3'
3717	8721		1.97	3.5E-01	AA642138.1	EST_HUMAN	m60d03.s1 NCI_CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172357 3'
4140	8135	14118	2.06	3.5E-01	AF071253.1	NT	Danio rerio homeobox protein (hoxb5b) gene, complete cds
4777	9761	14748	5.2	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
697	6721		1.44	3.4E-01	AJ242956.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
961	5976	11010	5.81	3.4E-01	Y09798.2	NT	Pseudomonas fluorescens colR, colS genes, of222 and partial InaA gene
1308	6304	11351	1.76	3.4E-01	Y00554.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2338	7312	12433	1.56	3.4E-01	D80909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
2832	7951	12668	0.8	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2832	7951	12969	0.8	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3078	8092	13108	1.04	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3088	8104	13119	7.39	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGB1) mRNA, complete cds
3268	8281	13303	1.07	3.4E-01	AF034862.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3453	8461	13488	4.36	3.4E-01	AF108835.1	NT	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3701	8705		2.49	3.4E-01	BF449010.1	EST_HUMAN	Tn94a01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15
3939	8937		1.48	3.4E-01	AA584198.1	EST_HUMAN	Q8UJ15 DJ18C9.1 ;
4509	9499	14478	1.77	3.4E-01	BE089912.1	EST_HUMAN	nc11b10.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4794	9778		4.55	3.4E-01	AI240973.1	EST_HUMAN	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
14	5094	10078	16.57	3.3E-01	X07990.1	NT	q95c05.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element
106	5094	10078	4.08	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
445	5482	10500	0.92	3.3E-01	AL161545.2	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
627	5655	10660	1.67	3.3E-01	7662485	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
1181	6183	11221	4.2	3.3E-01	Q12448	SWISSPROT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1288	6287	11331	3.14	3.3E-01	BF568890.1	EST_HUMAN	PROLINE-RICH PROTEIN LAS17
1569	6566	11628	1.18	3.3E-01	6753685	NT	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
							Mus musculus disintegrin 5 (Dign5), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1700	6895		2.03	3.3E-01	AA332734.1	EST_HUMAN	EST36722 Embryo, 8 week 1 Homo sapiens cDNA 5' and
1978	6963		1.4	3.3E-01	AF031148.1	NT	Methylococcus capsulatus strain Bath outer membrane protein MopB (mopB) gene, complete cds
							Homo sapiens uridine monophosphate synthetase (uridine phosphorylase) transferase and orotidine-5'-
							decarboxylase) (UMPS) mRNA
2340	7314		2.72	3.3E-01	4507834	NT	Bacteriophage phi-YeO3-12 complete genome
2878	7898	12821	1.78	3.3E-01	AJ251805.1	NT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION
							FACTOR 35 KD SUBUNIT) (CLMF P35)
2947	7866		0.67	3.3E-01	O02743	SWISSPROT	Streptomyces argillaceus mitramycin biosynthetic genes
2981	7899	13012	1.05	3.3E-01	AJ007832.2	NT	Homo sapiens MTA1-L1 gene, complete cds
3475	8424	13452	1.05	3.3E-01	AB012922.1	NT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3720	8724	13724	1.91	3.3E-01	O84845	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT
							PROTEINASE (HC-PRO); PROTEIN P3]
3727	8731	13728	1.01	3.3E-01	P22602	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3858	8860	13866	1.38	3.3E-01	AL161488.2	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
3895	8895	13893	1.71	3.3E-01	AF200446.1	NT	Homo sapiens RAS protein activator like 1 (GAP1 like) (RASAL1) mRNA
4168	9161		2.36	3.3E-01	4756025	NT	Rattus norvegicus DNA for regucalcin, partial cds
4242	9236		1.68	3.3E-01	D31682.1	NT	PEPTIDE TRANSPORTER 1 (HUMAN);
							PEPTIDE TRANSPORTER 1 (HUMAN);
4551	9538		1.7	3.3E-01	A1539114.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766
4690	9875	14658	1.36	3.3E-01	D64003.1	NT	ox0409.x1 Soares_fetal_liver_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655392 3' similar to
							contains element MER4 repetitive element :
5071	10040	15007	0.98	3.3E-01	A1021992.1	EST_HUMAN	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
454	5491		1.61	3.2E-01	AF018261.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
708	5732		0.78	3.2E-01	AL161561.2	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1144	6148		10.13	3.2E-01	AF047013.1	NT	P. vulgaris arc5-1 gene
1263	6261	11304	2.24	3.2E-01	Z50202.1	NT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1367	6364	11413	5.08	3.2E-01	Q48624	SWISSPROT	S. cerevisiae chromosome II reading frame ORF YBR172c
1737	6732	11809	1.1	3.2E-01	Z36041.1	NT	EST369284 MAGe resequences, MAGD Homo sapiens cDNA
1746	6741	11820	4.36	3.2E-01	AW957194.1	EST_HUMAN	EST369284 MAGe resequences, MAGD Homo sapiens cDNA
1746	6741	11821	4.36	3.2E-01	AW957194.1	EST_HUMAN	EST369284 MAGe resequences, MAGD Homo sapiens cDNA
2096	7077	12191	1.78	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2470	7438		2.59	3.2E-01	7710079	NT	Mus musculus Pbx/knotted 1 homeobox (Pbxox1), mRNA
2637	7597	12711	1.11	3.2E-01	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3046	8082	13070	1.07	3.2E-01	BF380745.1	EST_HUMAN	IL2-UT0073-180900-161-H11 UT0073 Homo sapiens cDNA

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4270	9263	14253	1.73	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4369	9362	14342	1.43	3.2E-01	Q10288	SWISSPROT	HYPOPHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME I PRECURSOR
4597	9585		7.8	3.2E-01	BF693617.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
5054	10025	14994	1.02	3.2E-01	AL181514.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 26
2600	7562	12680	2.32	3.1E-01	R18051.1	EST_HUMAN	ye90h08.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:M64241 QM PROTEIN (HUMAN);
2625	7709	12698	2.72	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2625	7709	12697	2.72	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2785	7806		1.27	3.1E-01	AW628036.1	EST_HUMAN	h146h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2875391 3'
3100	8116		3.43	3.1E-01	AB028069.1	NT	Mus musculus gene for Ser/Thr Kinase KKIAMPRE, exon 6
3811	8814	13820	0.89	3.1E-01	AJ251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
4806	9780	14772	5.69	3.1E-01	AE003984.1	NT	Xylella fastidiosa, section 130 of 229 of the complete genome
71	7689	10158	1.59	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Pkcε), mRNA
252	5312	10323	9.02	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1204	6205	11242	1.55	3.0E-01	AW300400.1	EST_HUMAN	xs63f08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1478	6475	11532	3.47	3.0E-01	AJ008755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
1760	6752	11837	1.03	3.0E-01	X98082.1	NT	A. immerus putative gene encoding integrase, Mars2 (RP)
3139	8155		4.06	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alypG gene for polyglutamate lyase, complete cds
3774	8777	13781	1.61	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0262-281199-001-g01 ST0262 Homo sapiens cDNA
3867	8868	13871	0.98	3.0E-01	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4362	9373	14352	2.28	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
4589	9577		0.99	3.0E-01	AF167835.1	NT	Bacteriophage APSE-1, complete genome
1973	6958	12063	1.16	2.9E-01	AE000736.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
3110	8126	13148	1.04	2.9E-01	AF078111.1	NT	Xenopus laevis transcription factor E2F mRNA, complete cds
3178	8194	13216	2.82	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171299-001-f12 CT0326 Homo sapiens cDNA
3178	8194	13217	2.82	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171299-001-f12 CT0326 Homo sapiens cDNA
3801	8804	13809	0.7	2.9E-01	AI610836.1	EST_HUMAN	lp21a11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 NIL-2-A
3959	8957	13946	12.27	2.9E-01	AB016426.1	NT	ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element;
4359	9350	14329	1.05	2.9E-01	AA284468.1	EST_HUMAN	Cavia porcellus mRNA for glutathione s-transferase, complete cds
4545	9534		0.85	2.9E-01	AL163207.2	NT	zs57412.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element;
						EST_HUMAN	Homo sapiens chromosome 21 segment HS21C007

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4946	9923		1.33	2.9E-01	AB670899.1	EST_HUMAN	w06f03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297309 3' similar to contains L1.12 L1 repetitive element ;
5020	9991		1.01	2.9E-01	AL161585.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 81
563	5597		2.11	2.8E-01	U67136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
568	5601		0.7	2.8E-01	U28145.1	NT	Ptarmica dwarf virus movement protein, complete cds; coat protein, complete cds
1067	6075	11108	2.54	2.8E-01	AF168050.1	NT	Guinea guinea oocyte maturation factor Mos (c-mos) gene, partial cds
1258	6256	11298	0.98	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1258	6268	11299	0.98	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1272	6270	11310	0.92	2.8E-01	D86550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1689	6885	11761	2.03	2.8E-01	AW860020.1	EST_HUMAN	QV1-CT0384-120200-065-b05 CT0384 Homo sapiens cDNA
1962	6948	12050	1.44	2.8E-01	AL047820.1	EST_HUMAN	DKFZp586i2321_r1 586 (synonym: hule1) Homo sapiens cDNA clone DKFZp586i2321
2073	7055	12165	1	2.8E-01	AW511195.1	EST_HUMAN	hd44b03.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2401	7372	12493	2.08	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2476	7445		1.49	2.8E-01	AL161585.2	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2594	7557	12671	1.4	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
2801	7820		1.35	2.8E-01	AF178480.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2802	7921	12941	2.3	2.8E-01	Z14037.1	NT	Toxoplasma gondii 80kDa heat-shock protein (HSP90) mRNA, partial cds
2802	7921	12942	2.3	2.8E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)
3294	8305	13330	0.85	2.8E-01	AP000004.1	NT	B.taurus microsatellite (ETH121)
3890	8890	13888	1.44	2.8E-01	AE001180.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt, position (47)
4005	9001		0.91	2.8E-01	AE004450.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4075	9089		2.36	2.8E-01	AI090868.1	EST_HUMAN	Pseudomonas aeruginosa PA01, section 11 of 529 of the complete genome
4337	9328	14313	2.15	2.8E-01	P13615	SWISSPROT	ov44g10.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1840226 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
4682	9667	14648	2.85	2.8E-01	AF030154.1	NT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4711	9698	14680	1.28	2.8E-01	BF628188.1	EST_HUMAN	Bovine adenovirus 3 complete genome
4731	9716	14701	2.3	2.8E-01	AI272669.1	EST_HUMAN	602042601F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4180129 5'
5004	9975	14950	1.68	2.8E-01	AA767084.1	EST_HUMAN	q159c11.x1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element ;
473	5509	10522	2.82	2.7E-01	Y17324.1	NT	ca41h01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1307569 3'
609	5836	10637	2.19	2.7E-01	AA450061.1	EST_HUMAN	Rattus norvegicus CDK104 mRNA
1242	6240	11281	1.67	2.7E-01	AB004908.1	NT	zx39b10.s1 Soares total testis_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element;
							Ipomoea purpurea transposable element T1p100 gene for transposase, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1582	6579		1.3	2.7E-01	X79815.1	NT	G.lamblii SR2 gene
1691	6687	11762	2.21	2.7E-01	W58087.1	EST_HUMAN	zz22h10.11 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1739	6734	11811	1.16	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2077	7762		1.42	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monoamine transporter, type 2, promoter region and exon 1
2306	7281	12389	6.34	2.7E-01	Y13868.1	NT	Feline immunodeficiency virus env gene, isolate ITT0088PIU (M88), partial
2386	7357	12479	2.78	2.7E-01	AJ310858.1	EST_HUMAN	la43c11.x2 NCL CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element;
2815	7834		0.72	2.7E-01	BF088284.1	EST_HUMAN	CM1-HT0875-060900-385-e05 HT0875 Homo sapiens cDNA
3904	8904	13902	1.98	2.7E-01	A928015.1	EST_HUMAN	w92e11.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
3918	8918	13911	2.28	2.7E-01	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
4739	9724	14709	1.14	2.7E-01	L27516.1	NT	Triticum aestivum (Wcs66) gene, complete cds
4875	9854		4.25	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-016-e03 CT0286 Homo sapiens cDNA
477	7721	10516	1.71	2.8E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
477	5514		1.09	2.8E-01	D18459.1	NT	Bos taurus mRNA for mb-1, complete cds
1370	6367	11416	1.36	2.6E-01	BE885087.1	EST_HUMAN	601510338F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1410	6408	11466	0.92	2.6E-01	AB013280.1	NT	Glycine max pseudogene for Bd 30K
1856	6845	11932	4.82	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1856	6845	11933	4.82	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
2037	7020		7	2.6E-01	AW733152.1	EST_HUMAN	bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14889_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2092	7073	12187	1.04	2.6E-01	M11844.1	NT	Human prealbumin gene, complete cds
2402	7373		3.5	2.6E-01	Y12896.1	NT	B. maritimus rbcL gene
2475	7444		5.05	2.6E-01	BE272440.1	EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2980043 5'
3018	8035		1.09	2.6E-01	AW974531.1	EST_HUMAN	EST386635 MAGe resequences, MAGM Homo sapiens cDNA
3558	8565	13572	2.15	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
3983	8981	13966	0.94	2.6E-01	AW859510.1	EST_HUMAN	EST371580 MAGe resequences, MAGF Homo sapiens cDNA
4031	8027	14016	17.72	2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA
4231	9225	14208	1.2	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4417	9407	14394	1.2	2.6E-01	AA457617.1	EST_HUMAN	aa89d07.r1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4512	9502	14481	2.55	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*) mRNA, complete cds

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Table 4

Single Exon Probes Expressed in HBL100 Cells							Top Hit Descriptor
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4577	8565	14553	1.48	2.6E-01	AF142703.1	NT	Ophrestia radicata maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
4812	9786	14779	3.7	2.6E-01	H04858.1	EST_HUMAN	y51e05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5'
4877	9856		1.53	2.6E-01	AA884625.1	EST_HUMAN	am33b11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1468605 3'
5089	10038	15005	1.24	2.6E-01	M37701.1	NT	P.chrysosporium lignin peroxidase genes, complete cds
239	5301	10311	1.57	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
240	5301	10311	2.3	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
253	5313		7.98	2.5E-01	M26501.1	NT	Starfish (P. ochiraceus) cytoplasmic actin gene, complete cds
822	5842	10878	0.98	2.5E-01	U09984.1	NT	Mus musculus ICR/Swiss glycerinaldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1043	6053		0.73	2.5E-01	AE002156.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1104	6111	11142	14.85	2.5E-01	T89837.1	EST_HUMAN	yel1g07.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117468 5'
1690	6686		3.61	2.5E-01	4885408	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1844	7757	11922	1.29	2.5E-01	BE696604.1	EST_HUMAN	PM4-CT0400-310700-005-008 CT0400 Homo sapiens cDNA
1844	7757	11923	1.29	2.5E-01	BE696604.1	EST_HUMAN	PM4-CT0400-310700-005-008 CT0400 Homo sapiens cDNA
2342	7318		6.55	2.5E-01	AE000875.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2565	7528	12846	1	2.5E-01	X95310.1	NT	B.taurus mRNA for D-aspartate oxidase
3328	8338		3.33	2.5E-01	AW973471.1	EST_HUMAN	EST385464 IMAGE resequences, MAGM Homo sapiens cDNA
3457	8485	13492	1.12	2.5E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3473	8481	13500	6.31	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3757	8760	13759	1.55	2.5E-01	A1741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3757	8760	13760	1.55	2.5E-01	A1741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3955	8953		1.09	2.5E-01	P32323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4191	9184		0.91	2.5E-01	Q03314	SWISSPROT	RHB PROTEIN
4606	9594		1.31	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MiH)
4611	9597	14583	4.87	2.5E-01	AF007768.1	NT	Charistoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4637	9622	14614	2.24	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4658	9643		3.61	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4722	9707	14694	0.8	2.5E-01	U83656.1	NT	Rattus norvegicus NF-KB gene, promoter region
549	5583	10585	1.12	2.4E-01	AA836316.1	EST_HUMAN	on70d04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
838	5857	10898	1.73	2.4E-01	BF576124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'
1285	6284	11326	14.3	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1285	6284	11327	14.3	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1814	6804		14.57	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1859	6848	11936	1.08	2.4E-01	AF251708.1	NT	Zaocys dhumnades fructose-1,6-bisphosphatase mRNA, complete cds
2104	7084		1.04	2.4E-01	AF45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2200	7178	12301	1.88	2.4E-01	AE000880.1	NT	Aquifex aolicus section 12 of 109 of the complete genome
2320	7295	12415	131.89	2.4E-01	BF002171.1	EST_HUMAN	7h23404.X1 NCI_CGAP_Cot6 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA
2467	7436	12553	2.1	2.4E-01	Z36634.1	NT	O42586 26S PROTEASE REGULATORY SUBUNIT 6A ;
2688	7646	12761	1.53	2.4E-01	X71783.1	NT	D.discoideum (Ax3-K) ponA gene
2713	7670	12783	3.6	2.4E-01	AF030154.1	NT	S.pombe swi6 gene
3059	8076		3.61	2.4E-01	U72726.1	NT	Bovine adenovirus 3 complete genome
3075	8091	13105	1.58	2.4E-01	X74209.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
3675	8680	13683	0.71	2.4E-01	AE000312.1	NT	H.sapiens AGT gene, PstI fragment of intron 4
3920	8920		0.95	2.4E-01	D29860.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4986	9960	14937	1.38	2.4E-01	AF282302.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
388	5426	10441	0.83	2.3E-01	S75898.1	NT	Oncorhynchus mykiss shaker-related potassium channel Tsh2 gene, complete cds
631	5659		4.7	2.3E-01	U39713.1	NT	aromatase [Poephilia guttata=zebra finches, ovary, mRNA, 3188 nt]
659	5686	10693	27.33	2.3E-01	U67596.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
921	5937	10968	3.41	2.3E-01	BE311893.1	EST_HUMAN	Melhanococcus jannaschii section 138 of 150 of the complete genome
1592	6588	11650	2.09	2.3E-01	Y10887.2	NT	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1894	6978		1.08	2.3E-01	AJ235333.1	NT	Mus musculus cdh5 gene, exon 1, partial
2378	7350	12470	1.58	2.3E-01	BE297718.1	EST_HUMAN	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene
2579	7542	12658	0.92	2.3E-01	M11319.1	NT	601175582F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2751	6382	11411	1.97	2.3E-01	AB015033.1	NT	Human erythropoietin gene, complete cds
2893	7912	12933	0.93	2.3E-01	AA601379.1	EST_HUMAN	Marniliabla agarovorans gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957
3010	8027		6.01	2.3E-01	R21732.1	EST_HUMAN	not6d06.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu
3216	8231	13252	0.91	2.3E-01	U66391.1	NT	repetitive element/contains element THR repetitive element ;
3288	8299	13326	1.23	2.3E-01	H69386.1	EST_HUMAN	Yh21b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
3832	8834		5.25	2.3E-01	7662133	NT	Lycopodium esculentum PRF (Prf) gene, complete cds
4224	9218	14197	6.38	2.3E-01	R82252.1	EST_HUMAN	Yh21b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4277	9270		1.85	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4328	9320	14305	0.87	2.3E-01	D90899.1	NT	Synechocystis sp. PCC6803 complete genome, 127, 1-133859
4360	9351	14330	2.08	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4422	9412	14400	5.79	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
4882	9861	14832	0.69	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
88	5165	10176	0.8	2.2E-01	AI052190.1	EST_HUMAN	oz14a10.x1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN ;
1532	6530	11560	2.42	2.2E-01	AF187850.1	NT	Homo sapiens PPAR delta gene, promoter region
1969	6954		1.16	2.2E-01	AF171901.1	NT	Trimeresurus malabaricus cyb gene, partial cds; mitochondrial gene for mitochondrial product
2035	7018	12128	1.86	2.2E-01	M34840.1	NT	Fresh-water sponge Emr1 alpha collagen (COLF1) gene
2339	7313	12434	4.2	2.2E-01	BF077538.1	EST_HUMAN	602085608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248969 5'
2512	7480	12595	1.38	2.2E-01	BE618258.1	EST_HUMAN	601482628F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868180 5'
2512	7480	12596	1.38	2.2E-01	BE618258.1	EST_HUMAN	601482628F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868180 5'
2812	7832	12848	5.48	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281289-003-at12 HT0353 Homo sapiens cDNA
2812	7832	12849	5.48	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281289-003-at12 HT0353 Homo sapiens cDNA
2850	7870		1.44	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3308	8319		2.3	2.2E-01	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
3687	8872	13676	1.51	2.2E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
3724	8728		1.61	2.2E-01	AF155728.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4091	9085		1.09	2.2E-01	AF119102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4098	9092	14078	6.31	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4141	9136	14119	2.24	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekkt1) mRNA, complete cds
4141	9136	14120	2.24	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekkt1) mRNA, complete cds
4230	9224	14208	1.24	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4230	9224	14207	1.24	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4879	9684		1.4	2.2E-01	D50804.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4884	9689	14851	2.15	2.2E-01	AA211216.1	EST_HUMAN	z887c05.11 Stralagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648968 5'
4878	9857		1.24	2.2E-01	L13289.1	NT	Mus musculus vinculin gene, exon 3
4961	9938	14915	0.91	2.2E-01	H60548.1	EST_HUMAN	y42h09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208001 5' similar to gb:Z14116_rna1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
956	5972	11006	1.5	2.1E-01	AA559289.1	EST_HUMAN	nm31e11.s1 NCI CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804
959	5974	11008	1.79	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit/Descriptor
1107	6113		2.15	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1179	6181	11217	1.22	2.1E-01	6754259	NT	Mus musculus Interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1179	6181	11218	1.22	2.1E-01	6754299	NT	Mus musculus Interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1869	6858	11946	1.52	2.1E-01	AA06824.1	EST_HUMAN	dk73e02.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519810 3' similar to gb:K02765
2094	7076	12189	2.42	2.1E-01	BF695073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
2854	7874	12889	2.25	2.1E-01	6912445	NT	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
3718	8722		6.22	2.1E-01	9838361	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3940	8938	13930	1.28	2.1E-01	P11875	SWISSPROT	Beta vulgaris mitochondrion, complete genome
3940	8938	13931	1.28	2.1E-01	P11875	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4128	9123		0.9	2.1E-01	AF124526.1	NT	Orchestia cavarana calcium-binding protein BP23 precursor (BP23) gene, complete cds
4251	9245		1.28	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4443	9433	14416	1.68	2.1E-01	AB010273.1	NT	Homo sapiens pshsp47 gene, complete cds
4719	9704	14690	4	2.1E-01	AJ009794.1	NT	Homo sapiens hox11 proto-oncogene, exons 1 to 3 end hug-1 gene
5030	10001		0.92	2.1E-01	P26680	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN) (P22); ENVELOPE GLYCOPROTEIN E1 (GP32) (GP35); ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70) (NS1); PROTEIN P7; NONSTRUCTURAL PROTEIN NS2 (P21); PROTEINASE/HELICASE NS3 (P70); NONSTRUCTURAL PROTEIN>
5067	10036	15003	1	2.1E-01	U02948.1	NT	Human surfactant protein-C (SP-C) gene, complete cds
200	5264	10278	2.64	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avena, complete cds
530	5565		2.17	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
650	5714	10728	1.32	2.0E-01	M77085.1	NT	O. cumiculus germline lgh heavy chain V-H pseudogene, allotype VH2
801	5822	10862	5.78	2.0E-01	AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region
988	6008	11038	0.68	2.0E-01	D90905.1	NT	Synechocystis sp. PCC6803 complete genome, 7/27, 781449-920915
1108	6114	11144	2.91	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1235	6233	11277	1.34	2.0E-01	AJ132695.5	NT	Homo sapiens rec1 gene
1289	6288	11332	1.08	2.0E-01	AW384937.1	EST_HUMAN	PM1-HT0422-291289-002-c06 HT0422 Homo sapiens cDNA
1432	6429		1.01	2.0E-01	AJ243957.1	NT	Plum pox virus strain M, complete genome, isolate PS
1456	6453	11512	7.19	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1520	6517	11574	3.81	2.0E-01	AB007874.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
1626	6523	11580	1.54	2.0E-01	AF260700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1658	6654	11726	1.48	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1879	6875		1.48	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jaggd2 gene, complete cds; and unknown gene

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1720	6715		3.88	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1853	6842	11830	0.93	2.0E-01	8922238	NT	Homo sapiens hypothetical protein FLJ10120 (FLJ10120), mRNA
2288	7262		1.21	2.0E-01	X82877.1	NT	H. sapiens Na ⁺ -D-glucose cotransport regulator gene
3407	8418	13444	0.68	2.0E-01	P46607	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3489	8487		0.67	2.0E-01	AW238005.1	EST_HUMAN	xp15b02.x1 NCL_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740385 3' similar to contains element
3624	8631	13637	0.7	2.0E-01	P34641	SWISSPROT	MER21 repetitive element ;
3919	8919	13912	0.77	2.0E-01	X83897.1	NT	C.parasitica eapC gene
4433	9423		9.72	2.0E-01	BE826165.1	EST_HUMAN	QV4-EN0032-190500-223-603 EN0032 Homo sapiens cDNA
4874	9853	14828	7.34	2.0E-01	8922080	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
4931	9908	14885	0.93	2.0E-01	Y19216.1	NT	Homo sapiens putative psihHbD pseudogene for hair keratin, exons 1 to 9
4979	7840		7.48	2.0E-01	AF074990.1	NT	Homo sapiens full length insert cDNA YH85A11
5045	10016	14985	1.19	2.0E-01	AF187169.1	NT	Mus musculus cubilin mRNA, partial cds
5059	10029		1.29	2.0E-01	T47785.1	EST_HUMAN	yb17at0.1 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:71418 5'
110	5182		9.3	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Arnt1), mRNA
350	5402	10412	5.34	1.9E-01	AF004353.1	NT	Mus musculus pala ear (ep) gene, wild type allele, 3' region, partial cds
648	5976	10882	24.68	1.9E-01	U32581.2	NT	Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds
648	5976	10883	24.68	1.9E-01	U32581.2	NT	Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds
655	5983	10690	6.04	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
658	5983	10690	5.32	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
971	5986		0.98	1.9E-01	7305180	NT	Mus musculus Interleukin 2 receptor, gamma chain (IL2rg), mRNA
1087	6094	11124	12.01	1.9E-01	AA358813.1	EST_HUMAN	EST67784 Fetal lung II Homo sapiens cDNA 5' end
1353	6350	11400	3.22	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1409	6407		2.64	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2319	7294	12414	2.22	1.9E-01	8922533	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2852	7872	12887	3.91	1.9E-01	U60665.1	NT	Sigmatodon hispidus p53 gene, partial cds
2868	7887		5.5	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3311	8322	13346	4.28	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3359	8408	13434	4.85	1.9E-01	R16407.1	EST_HUMAN	yf42f10.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:129547 5'
3716	8720	13721	0.77	1.9E-01	AF264017.1	NT	Rattus norvegicus acylamide deacetylase gene, complete cds
3746	8750	13749	1	1.9E-01	P38768	SWISSPROT	PAIR-RULE PROTEIN ODD-PAIRED
3886	8887	13886	3.37	1.9E-01	AB008784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
3968	8967	13956	1.47	1.9E-01	AW754106.1	EST_HUMAN	CIM3-CT0315-271189-045-511 CT0315 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4110	9104	14080	1	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-280700-007-404 FN0010 Homo sapiens cDNA
4851	9833		1.11	1.9E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
32	5112	10098	1.73	1.8E-01	U73200.1	NT	Mus musculus p118Rip mRNA, complete cds
258	7717	10327	1.97	1.8E-01	AB022090.1	NT	Mus musculus Ccrg gene for chaperonin containing TCP-1 gamma subunit, partial cds
369	5418	10433	1.48	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
737	5760	10783	1.61	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
967	5982	11014	0.75	1.8E-01	AI912212.1	EST_HUMAN	wf71f02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1075	6082	11112	1.17	1.8E-01	AF000580.1	NT	Dicotyledon discoidium plasmid Ddp5, complete genome
1269	6267	11309	7.26	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1810	6800		1.18	1.8E-01	4505038	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1828	6819		1.34	1.8E-01	AI733708.1	EST_HUMAN	q922410.x5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O75936 O75936 GAMMA BUTYROBETAINE HYDROXYLASE ;
1871	6860	11948	1.42	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2820	7582		1.63	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT0018-081299-038-g04 DT0018 Homo sapiens cDNA
2827	7848		1.6	1.8E-01	AF184589.1	NT	Jonopsidium acaule LEAFY protein (LEAFY2) gene, partial cds
2833	7853	12873	1.28	1.8E-01	AW182300.1	EST_HUMAN	X41a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659756 3'
3051	8068	13077	2.5	1.8E-01	AW985178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3285	8286	13322	0.68	1.8E-01	BF183582.1	EST_HUMAN	601809723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040821 3'
3540	8546	13553	0.78	1.8E-01	H03369.1	EST_HUMAN	y45601.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
3540	8546	13554	0.78	1.8E-01	H03369.1	EST_HUMAN	y45601.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
4206	9199		1.21	1.8E-01	D37854.1	NT	Bovine NB25 mRNA for MHC class II (BoLA-DQB), complete cds
4424	9414	14401	5.34	1.8E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4627	9612	14601	3.53	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
4661	9846	14634	1.89	1.8E-01	X92179.1	NT	S.tuberosum mRNA for alcohol dehydrogenase
4880	9859	14830	2.79	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151299-112-g08 ST0203 Homo sapiens cDNA
4924	9901	14877	6.38	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
4942	9919	14899	1.04	1.8E-01	AI439881.1	EST_HUMAN	h57e04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5081	10030	14997	0.93	1.8E-01	X60208.1	NT	Escherichia coli reverse transcriptase, retron EC86
5081	10030	14998	0.93	1.8E-01	X60208.1	NT	Escherichia coli reverse transcriptase, retron EC86
572	6605	10603	1.66	1.7E-01	BE385184.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
798	5917	10848	1.92	1.7E-01	X53330.1	NT	P.dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
946	5983		2	1.7E-01	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1041	6051	11080	1.31	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolydnavirus, complete genome
1041	6051	11081	1.31	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolydnavirus, complete genome
1781	6773	11865	1.64	1.7E-01	AL181573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
1835	6921		1.96	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2788	7809	12828	2.05	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpl) gene, partial cds, hemagglutinin/protease regulatory protein (hpr) gene, complete cds, and YRAL VIBCO gene, partial cds
2788	7809	12827	2.05	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpl) gene, partial cds, hemagglutinin/protease regulatory protein (hpr) gene, complete cds, and YRAL VIBCO gene, partial cds
2856	7876	12892	1.55	1.7E-01	AA336909.1	EST_HUMAN	EST41851 Endometrial tumor Homo sapiens cDNA [5' end
2928	7947	12894	1.1	1.7E-01	AJ238736.1	NT	Naja naja atra cdx-1 gene, exons 1-3
2928	7947	12895	1.1	1.7E-01	AJ238736.1	NT	Naja naja atra cdx-1 gene, exons 1-3
3032	8049	13058	1.45	1.7E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3363	8371	13391	1.56	1.7E-01	AJ269505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpC gene, adpD gene, adpE gene and adpF gene
3527	8533	13540	1.17	1.7E-01	AJ224877.1	NT	Homo sapiens hap1 gene, complete CDS
3836	8837	13843	6.17	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/TEL gene
4428	8418		1.89	1.7E-01	X52936.1	NT	Schistocerca gregaria alpha repetitive DNA
4691	9676	14659	1.31	1.7E-01	AI247835.1	EST_HUMAN	q157609.x1 Scores fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 ORF repetitive element ;
4932	9809	14988	8.78	1.7E-01	AB007841.1	NT	Homo sapiens mRNA for KIAA0472 protein, partial cds
126	5194	10208	1.54	1.6E-01	AF217532.1	NT	Homo sapiens mevalonate kinase gene, exon 6 and 7
671	7695	10705	1.11	1.6E-01	R31497.1	EST_HUMAN	Y17512.1 Scores placenta N52HP Homo sapiens cDNA clone IMAGE:135599 5'
1474	8471	11529	1.07	1.6E-01	AA548863.1	EST_HUMAN	nk28d12.s1 NCL_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014839 3'
1490	8487	11542	2.68	1.6E-01	AF298117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1883	8872	11961	1.19	1.6E-01	P22083	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
1938	6924		1.08	1.6E-01	U10334.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2322	7768	12418	0.98	1.6E-01	X94232.1	NT	H.sapiens mRNA for novel T-cell activation protein
2421	7393	12514	1.22	1.6E-01	AB037729.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2822	7842	12859	10.97	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2821	7842	12860	10.97	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3548	8555	13562	1.16	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3548	8555	13563	1.16	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3685	8699	13692	0.73	1.6E-01	AE000962.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
3894	8894	14177	2.51	1.6E-01	AF179880.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of this complete chromosome
4202	9195	14177	10.56	1.6E-01	AF179880.1	NT	Homo sapiens apelin gene, complete cds
4334	9325	14177	2.61	1.6E-01	AW968601.1	EST_HUMAN	EST380677 MAGI resequences, MAGJ Homo sapiens cDNA
4340	9331		3.9	1.6E-01	6753319	NT	z84h09.s1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221855
4788	9772	14755	1.47	1.6E-01	AA088343.1	EST_HUMAN	E221855 38,855 BP SEGMENT OF CHROMOSOME XIV.:
4810	9794	14776	1.19	1.6E-01	AJ006356.1	NT	Lycopodium obscurum RsaI fragment 2, satellite region
4810	9794	14777	1.19	1.6E-01	AJ006356.1	NT	Lycopodium obscurum RsaI fragment 2, satellite region
							LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 PRECURSOR (MEGALIN)
5029	10000	14973	1.21	1.6E-01	P98158	SWISSPROT	(GLYCOPROTEIN 330)
246	5308	10316	1.38	1.5E-01	BE110087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
246	5308	10317	1.38	1.5E-01	BE110087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
582	7694		2.11	1.5E-01	AV711696.1	EST_HUMAN	AV711696 DCA Homo sapiens cDNA clone DCAADH05 5'
774	5798	10824	1.39	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1080	6087	11116	1.81	1.5E-01	AJ251885.1	NT	Homo sapiens partial SLG2A2 gene for organic cation transporter (OCT2), exon 1
1096	6103		2.69	1.5E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1197	6198	11234	0.7	1.5E-01	AW195516.1	EST_HUMAN	xn39d11.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2696085 3'
1256	6254	11295	2.85	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1256	6254	11298	2.85	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1451	6448	11509	1.47	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
2639	7599	12713	1.34	1.5E-01	BF695381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
							xw59a02.x2 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb:X55072_ma1
2843	7863		1.06	1.5E-01	AW572516.1	EST_HUMAN	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);
3274	8286	13310	4.64	1.5E-01	AA935049.1	EST_HUMAN	cc68405.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
							RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN);
3670	8675	13678	2.01	1.5E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3684	8688	13691	1.04	1.5E-01	7108358	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3775	8778	13782	2.39	1.5E-01	AW665983.1	EST_HUMAN	h10f06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
3937	8936	13929	0.86	1.5E-01	AW366659.1	EST_HUMAN	RC2-HT0149-19T099-012-c08 HT0149 Homo sapiens cDNA
4059	9053	14040	8.83	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C08+
4585	9573	14563	1.41	1.5E-01	BF687665.1	EST_HUMAN	602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066223 5'
4607	7599	12713	2.83	1.5E-01	BF695381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
4840	9824	14789	1.66	1.5E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
297	5354		1.51	1.4E-01	AF008663.1	NT	Homo sapiens T cell receptor beta locus, TCRBV85P to TCRBV21S2A2 region
899	5917		2.72	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1240	6238		2.11	1.4E-01	T91884.1	EST_HUMAN	y454c01.s1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:112032 3'
1709	6704		1.2	1.4E-01	6678980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1712	6707	11783	1.61	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
1939	6925		8.74	1.4E-01	AA720615.1	EST_HUMAN	ny72a07.s1 NCI_CGAP_GCBT Homo sapiens cDNA clone IMAGE:1283821 3'
2720	7677	12791	4.16	1.4E-01	A1933466.1	EST_HUMAN	wm74d01.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'
3464	8472		1.55	1.4E-01	BF341524.1	EST_HUMAN	602013527F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4149126 5'
3803	8806	13811	1.17	1.4E-01	R59232.1	EST_HUMAN	y97a03.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41487 5'
3803	8806	13812	1.17	1.4E-01	R59232.1	EST_HUMAN	y97a03.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41487 5'
4050	9046	14034	11.16	1.4E-01	A1699094.1	EST_HUMAN	b56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4050	9046	14035	11.16	1.4E-01	A1699094.1	EST_HUMAN	b56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4115	9109	14094	3.6	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
320	5375	10384	2.28	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
320	5375	10385	2.28	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
525	5560	10563	1.88	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
630	5658	10663	1.51	1.3E-01	AJ277606.1	NT	Human calicivirus HUINLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUINLV/Girlington/93/UK
630	5658	10664	1.51	1.3E-01	AJ277606.1	NT	Human calicivirus HUINLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUINLV/Girlington/93/UK
834	5853	10893	0.93	1.3E-01	X63330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
883	5901	10942	1.49	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1010	6020	11049	1.51	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1110	6116		2.67	1.3E-01	AL115265.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1196	6197	11233	1.71	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAFF05 5'
1418	6415		0.91	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1918	6906	11999	1.66	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2106	7086		0.97	1.3E-01	AJ243578.1	NT	Rhodospseudomonas acidophila pucB5, pucA5, pucB6, pucA7, pucB7, pucA8 and pucC genes and ORF151
2228	7205		1.04	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191089-032-d12 ST0173 Homo sapiens cDNA
2318	7293		2.79	1.3E-01	AE001018.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2510	7478	12593	1.78	1.3E-01	M89918.1	NT	Carassius auratus keralin type I mRNA, complete cds
3278	8260	13315	0.98	1.3E-01	AF198779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
3368	8376	13396	1.03	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolyl transacylase mRNA, complete cds
3639	8645	13651	0.81	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3639	8645	13652	0.81	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3882	8883		1.37	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
3938	5658	10663	1.73	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
3938	5658	10664	1.73	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
4016	9012		0.82	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4034	9030		4.19	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081289-036-a03 DT0018 Homo sapiens cDNA
4042	9038	14028	1.79	1.3E-01	AF028805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4061	9055	14042	18.31	1.3E-01	AW273741.1	EST_HUMAN	xx23f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4187	9180		1.38	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4403	9394	14378	2.77	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'
4940	8917	14897	1.76	1.3E-01	A1432531.1	EST_HUMAN	th38c10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2120562 3'
382	5457	10474	9.01	1.2E-01	A1421744.1	EST_HUMAN	H39502.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_rna1
421	5078		1.74	1.2E-01	U66912.1	NT	ANNEXIN V (HUMAN);
543	5577		2.9	1.2E-01	AF039442.1	NT	Dictyostellum discoideum ORF DG1016 gene, partial cds
1358	6355	11405	2.5	1.2E-01	AU149146.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1358	6355	11406	2.5	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1364	6361		3.56	1.2E-01	AV735249.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1477	6474		1.03	1.2E-01	AA897474.1	EST_HUMAN	AV735249 cda Homo sapiens cDNA clone cdaAUB11 5'
							el48e09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671
							Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1591	6587	11649	1.16	1.2E-01	Q14934	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
1611	6607	11671	2.24	1.2E-01	AI285402.1	EST_HUMAN	q169f09.x1 NCI_CGAP_Eso2 Homo sapiens cDNA, clone IMAGE:1860553 3'
1731	6726		9.87	1.2E-01	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
1876	6885		3.06	1.2E-01	AW449368.1	EST_HUMAN	UIH-B13-aki-e-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2118	7098	12211	2.31	1.2E-01	BF248490.1	EST_HUMAN	601821567F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5'
2514	7482	12598	1.4	1.2E-01	AW996556.1	EST_HUMAN	QV3-BN0046-220300-129-f10 BN0046 Homo sapiens cDNA
2769	7790	12812	1.4	1.2E-01	U18018.1	NT	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2832	7852	12872	2.31	1.2E-01	AI720470.1	EST_HUMAN	as80c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L05095
2894	7894	12804	3.25	1.2E-01	M18364.1	NT	60S RIBOSOMAL PROTEIN L30 (HUMAN).
2936	7955	12973	0.9	1.2E-01	X56882.1	NT	Human creatine kinase-B mRNA, complete cds
3159	8175	13188	1.63	1.2E-01	AW370668.1	EST_HUMAN	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3183	8199		0.79	1.2E-01	U67600.1	NT	QV1-BT0259-261059-021-405 BT0259 Homo sapiens cDNA
3442	8450	13476	0.67	1.2E-01	X56882.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3442	8450	13477	0.67	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3525	8407		0.71	1.2E-01	Z99118.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
4058	9052	14038	1.91	1.2E-01	Z54255.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2785131 to 3013540
4058	9052	14039	1.91	1.2E-01	Z54255.1	NT	P. clarkii mRNA; repeat region (ID 2MRT7)
4848	9633		0.92	1.2E-01	AF221633.1	NT	P. clarkii mRNA; repeat region (ID 2MRT7)
4857	9838	14811	9.45	1.2E-01	BF577357.1	EST_HUMAN	Rana ridibunda pituitary adenylate cyclase-activating polypeptide variant 2 precursor, mRNA, complete cds, alternatively spliced
4937	9914	14892	3.98	1.2E-01	AL163227.2	NT	602135185F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4290165 5'
4937	9914	14893	3.98	1.2E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
5037	10027		4.85	1.2E-01	Q67599	SWISSPROT	Homo sapiens chromosome 21 segment HS21C027
560	5584	10594	0.74	1.1E-01	AI561003.1	EST_HUMAN	RIBONUCLEASE H1 (RNASE H1)
611	5638	10640	6.71	1.1E-01	AA569006.1	EST_HUMAN	ln18d08.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167983 3'
1037	6047	11077	1.16	1.1E-01	BF697308.1	EST_HUMAN	nm08g11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06985_rna1
1069	6077		1.46	1.1E-01	AL161560.2	NT	HEME OXYGENASE 1 (HUMAN);
1141	7740	11177	3.28	1.1E-01	AW972158.1	EST_HUMAN	602129847F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4288771 5'
1230	6229	11274	1.76	1.1E-01	D64004.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1488	6485	11540	1.79	1.1E-01	AU140363.1	EST_HUMAN	EST384142 IMAGE resequences, MAGL Homo sapiens cDNA
2250	7227		2.31	1.1E-01	6755216	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002985
							AU140363 PLAGE2 Homo sapiens cDNA clone PLAGE2000403 5'
							Mus musculus pre T-cell antigen receptor alpha (P1cra), mRNA

Table 4

Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2468	7707		1.24	1.1E-01	6978676	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2782	7803	12820	1.07	1.1E-01	S82418.1	NT	Interleukin-12 p35 subunit [mouse, Genomic, 700 nt, segment 4 of 5]
2983	7981	12995	0.83	1.1E-01	F03285.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
3267	8280		1.57	1.1E-01	6763231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Ca _v 1g), mRNA
3336	8346	13364	2.75	1.1E-01	BE393188.1	EST_HUMAN	601308676F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3369	8377	13397	1.5	1.1E-01	X62135.1	NT	C.reinhardtii nuclear gene on linkage group XIX
3411	8420	13449	1.26	1.1E-01	R95946.1	EST_HUMAN	y62g08 s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains
3501	8509	13523	0.8	1.1E-01	Y07695.1	NT	Alu repetitive element;
3619	8626		0.84	1.1E-01	P97384	SWISSPROT	A.limmerus gene for transposase
3627	8634	13639	1.44	1.1E-01	X52708.1	NT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
3994	8991	13975	1.01	1.1E-01	AW819412.1	EST_HUMAN	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
3994	8991	13976	1.01	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-280100-025-g07 ST0290 Homo sapiens cDNA
4131	9126		9.98	1.1E-01	AF167066.1	NT	MR3-ST0290-280100-025-g07 ST0290 Homo sapiens cDNA
4505	9495	14473	0.96	1.1E-01	S44957.1	NT	MR3-ST0290-280100-025-g07 ST0290 Homo sapiens cDNA
4685	9670	14652	1.09	1.1E-01	Y07696.1	NT	Drosophila melanogaster kirsicht protein (klar) mRNA, complete cds
4856	9837		0.86	1.1E-01	AW026547.1	EST_HUMAN	Tapa-1=Integral membrane protein TAPA-1 [mouse, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
5002	9973		1	1.1E-01	8923317	NT	A.limmerus gene for transposase
1182	6184		3.86	1.0E-01	O62855	SWISSPROT	wv14h02.x1 NCJ_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529555 3'
1253	6251	11292	1.81	1.0E-01	A1885499.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20342 (FLJ20342), mRNA
1369	6366	11415	1.69	1.0E-01	AL161504.2	NT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
3434	8442	13468	0.99	1.0E-01	BF033991.1	EST_HUMAN	ws08d01.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.13
3637	8643	13649	0.87	1.0E-01	BF239818.1	EST_HUMAN	MER7 repetitive element;
3848	8850	13858	2.47	1.0E-01	BF365703.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
4283	9275	14263	1.88	1.0E-01	AE002265.2	NT	601456301F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859849 5'
4423	9413		1.85	1.0E-01	A1792349.1	EST_HUMAN	601806489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
4574	9562	14550	1.74	1.0E-01	U50450.1	NT	QV2-NT0048-160800-316-e05 NT0048 Homo sapiens cDNA
4787	9751	14740	2.04	1.0E-01	AW952344.1	EST_HUMAN	Chlamydomonas reinhardtii AR39, section 91 of 94 of the complete genome
4967	9944	14921	0.93	1.0E-01	AL163247.2	EST_HUMAN	an32c04.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
5022	9993		3.42	1.0E-01	BE881566.1	EST_HUMAN	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
2714	7671	12784	1.21	9.9E-02	BE545554.1	EST_HUMAN	EST364414 IMAGE resequencing, MAGB Homo sapiens cDNA
2714	7671	12785	1.21	9.9E-02	BE545554.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
							601490280F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3892842 5'
							601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
							601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3192	8208	13229	1.36	9.9E-02	AF09810.1	NT	Homo sapiens neuraxin III-alpha gene, partial cds
559	5593		1.41	9.8E-02	X58338.1	NT	O. sativa RAmY3C gene for alpha-amylase
3072	8088	13101	4.03	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4102	8096	14081	5.22	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
4102	8098	14082	5.22	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
1332	6330	11379	1.38	9.7E-02	AB005808.1	NT	Alcea arborescens mRNA for NADP-malic enzyme, complete cds
1550	6547		1.11	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (echondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2199	7177	12300	1.44	9.7E-02	BE168660.1	EST_HUMAN	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA
3875	8876		3.83	9.7E-02	Q99785	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
1966	6951	12054	0.92	9.6E-02	A1080721.1	EST_HUMAN	0247411.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
1966	6951	12055	0.92	9.6E-02	A1080721.1	EST_HUMAN	0247411.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4219	9212	14191	5.54	9.6E-02	Z32686.2	NT	Proteus mirabilis fimbrial operon, strain HI4320
4842	9825	14800	1.16	9.6E-02	AW966230.1	EST_HUMAN	EST378303 MAGE rescues, MAGI Homo sapiens cDNA
4972	8948	14926	0.97	9.6E-02	BE061728.1	EST_HUMAN	RC5-BT0254-031099-011-a03 BT0254 Homo sapiens cDNA
3985	8983	13969	2.27	9.5E-02	AW992395.1	EST_HUMAN	CM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA
4947	8924	14902	0.93	9.5E-02	U63374.1	NT	Lycopodium esculentum polygalacturonase isoenzyme 1 beta subunit gene, complete cds
1797	6788	11877	2.69	9.4E-02	BF871083.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291917 5'
3788	8791	13798	5.14	9.4E-02	Z33059.1	NT	M. capricornum DNA for CONTIG MC073
2820	7939		1.7	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
2859	7978		6.91	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3182	8198	13222	2.33	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4029	9025	14012	3.03	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4029	9025	14013	3.03	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4595	9583		2.31	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5'
228	5291	10287	7.76	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
228	5291	10288	7.76	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
228	5291	10289	7.76	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2166	7145		3.57	9.2E-02	R54156.1	EST_HUMAN	y9807.r1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:41618 5'
3106	8122	13140	3.95	9.2E-02	Q28831	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3233	8248	13269	0.82	9.2E-02	AA534354.1	EST_HUMAN	n179807.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:926136 3'
3505	8513		1.08	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA
4116	9110		0.98	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4181	9174		0.72	9.2E-02	BE298722.1	EST_HUMAN	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960178 5'

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4504	9494	14472	1.99	9.2E-02	X96402.1	NT	G.gallus Mir-CK gene
420	5078	10063	6.08	9.1E-02	X77685.1	NT	O. cuniculus k12 keratin gene
3585	8592		0.93	9.1E-02	AW372588.1	EST_HUMAN	PM2-BT0349-161289-001-f02 BT0349 Homo sapiens cDNA
4357	9348	14328	1.84	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
735	5758	10780	4.53	9.0E-02	P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1594	6590	11651	5.3	9.0E-02	BE220482.1	EST_HUMAN	hV39g10.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element;
2731	7688	12802	2.97	9.0E-02	AF138522.1	NT	HIV-1 p8c095-08 from USA envelope glycoprotein (env) gene, partial cds
2731	7688	12803	2.97	9.0E-02	AF138522.1	NT	HIV-1 p8c095-08 from USA envelope glycoprotein (env) gene, partial cds
3262	8275	13299	0.76	9.0E-02	AF278135.1	NT	Dictyostelium discoideum spore coat structural protein SP65 (colE) gene, complete cds
4175	8169	14157	0.87	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4175	8169	14158	0.87	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4284	9286	14274	0.91	9.0E-02	P55288	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
4533	9523	14510	2.08	9.0E-02	X6740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
5028	8989	14972	1.01	9.0E-02	Q24597	SWISSPROT	REGULATORY PROTEIN ZESTE
1411	6409	11467	1.4	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1411	6409	11468	1.4	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
4076	9070		2.28	8.9E-02	AF286055.1	NT	Atrichum angustatum AtranFlo2 protein (AtranFlo2) gene, partial cds
1355	6352	11402	1.5	8.8E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3807	8810	13816	1.16	8.8E-02	AA299128.1	EST_HUMAN	EST11595 Uterus Homo sapiens cDNA 5' end
							TRANSCRIPTION INITIATION FACTOR TFIIID 135 KDA SUBUNIT (TAFII135) (TAFII-130) (TAFII130)
3924	8924		3.83	8.8E-02	O00268	SWISSPROT	ox65b01.s1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1661161 3'
1608	6604	11667	1.11	8.7E-02	AI167281.1	EST_HUMAN	
3610	8617	13826	4.63	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3610	8617	13627	4.63	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4568	8558	14544	1.24	8.7E-02	AF178636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
4928	8908		1.08	8.7E-02	AE000895.1	NT	Methanobacterium thermoautotrophicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1233	6231	11275	6.22	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2182	7161	12281	1.3	8.6E-02	BE408667.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3114	8130	13149	3.35	8.6E-02	L05468.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds
3559	8568		3.97	8.6E-02	AF153362.1	NT	Dichoselium discoidium adenyl cyclase (acrA) gene, complete cds
2333	7307	12428	1.85	8.6E-02	AF153362.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
2596	7776	12874	3.69	8.4E-02	AE000652.1	EST_HUMAN	z444e11.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343532 5'
4228	9222	14202	0.99	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
4228	9222	14203	0.99	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
3512	8520	13532	5.85	8.3E-02	P75334	SWISSPROT	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
4559	9547	14532	0.83	8.3E-02	AB038490.1	NT	Homo sapiens gene for fukutin, complete cds
1360	6357		6.17	8.2E-02	Y08170.2	NT	Gallus gallus mRNA for OBCAM protein gamma isoform
1465	6462	11521	2.51	8.2E-02	AF167077.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3000	8018		2.44	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
3713	8717		1.37	8.2E-02	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3901	8901	13889	1.16	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4161	9156	14139	5.75	8.2E-02	P48980	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4161	9156	14140	5.75	8.2E-02	P48980	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4161	9156	14141	5.75	8.2E-02	P48980	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4809	9888	14861	3.34	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5027	9998	14971	1.29	8.2E-02	AU118830.1	EST_HUMAN	AU118830 HEMBA1 Homo sapiens cDNA clone HEMBA1006744 5'
1464	6461	11520	1.06	8.1E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcI, and mdcM genes), complete cds
5062	10031	14999	1.05	8.1E-02	AE004673.1	NT	Pseudomonas aeruginosa PA01, section 234 of 525 of the complete genome
6	7711	10072	4.12	8.0E-02	AW854653.1	EST_HUMAN	EST366723 MAGC resequences, MAGC Homo sapiens cDNA
1659	7752	11728	9.29	8.0E-02	D28535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1659	7752	11728	9.29	8.0E-02	D28535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1862	6851	11939	2.81	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-508 BT0347 Homo sapiens cDNA
2400	7371		2.76	8.0E-02	AL445067.1	EST_HUMAN	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'
2830	7850	12869	0.67	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome; segment 5/5
3726	8730	13728	0.73	8.0E-02	AW966118.1	EST_HUMAN	EST378191 MAGC resequences, MAGC Homo sapiens cDNA
3958	8856		0.76	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
4631	9616	14607	1.25	8.0E-02	AK34202.1	EST_HUMAN	h31g02.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132114 3'
4669	9654		7.08	8.0E-02	X72794.1	NT	M.musculus gene for gelatinase B
5060	5939	10971	0.67	8.0E-02	U60315.1	NT	Mollusum contagiosum virus subtype 1, complete genome

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2109	7089	12203	2.54	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959510 5'
2910	7929	12948	11.99	7.9E-02	A1582029.1	EST_HUMAN	ar96c08.x1 Baresad colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:Z28876
3760	8763	13763	5.05	7.9E-02	6681044	NT	60S RIBOSOMAL PROTEIN L38 (HUMAN);
3760	8763	13764	5.05	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4666	9651		1.4	7.9E-02	AB006019.1	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
							Arabidopsis thaliana RXW24L mRNA, partial cds
1191	6192	11228	1.59	7.8E-02	A1793275.1	EST_HUMAN	cc59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570487 5' similar to contains L1.13 L1 repetitive element;
							cc59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570487 5' similar to contains L1.13 L1 repetitive element;
1191	6192	11229	1.59	7.8E-02	A1793275.1	EST_HUMAN	Sus scrofa telomerase RNA pseudogene
2332	7306	12426	1	7.8E-02	AF221942.1	NT	Sus scrofa telomerase RNA pseudogene
2332	7306	12427	1	7.8E-02	AF221942.1	NT	Sus scrofa telomerase RNA pseudogene
3663	8668		1.25	7.8E-02	BE250048.1	EST_HUMAN	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5'
4914	8668		3.15	7.8E-02	BE250048.1	EST_HUMAN	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5'
							Ig48g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112070 3' similar to contains MER10.13 MER10 repetitive element;
5068	10035	15002	1.02	7.8E-02	A1418520.1	EST_HUMAN	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
3508	8514		2.61	7.7E-02	AJ238093.1	NT	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3834903 5'
3303	8314	13340	2.57	7.6E-02	BE514432.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
3324	8334	13354	0.82	7.6E-02	AA286447.1	EST_HUMAN	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
776	5798	10826	1.86	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
776	5798	10827	1.86	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1877	6866	11954	1.16	7.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4377	8368	14348	0.92	7.5E-02	AB015961.1	NT	Homo sapiens IL-18 gene for Interleukin-18, intron 1 and exon 2
474	5510	10523	1.1	7.4E-02	AW838547.1	EST_HUMAN	RCS-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
3514	8522	13533	0.77	7.4E-02	A1807885.1	EST_HUMAN	wf43101.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356385 3'
4566	9554	14541	1.18	7.4E-02	L78810.1	NT	Homo sapiens ADPIATP carrier protein (ANT-2) gene, complete cds
4650	9635	14628	2.97	7.4E-02	6978442	NT	Rattus norvegicus Activin receptor like kinase 1 (Actv11), mRNA
4784	9788	14762	1.75	7.4E-02	6878492	NT	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchrrp), mRNA
466	5503	10514	1.23	7.3E-02	BE94991.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
466	5503	10515	1.23	7.3E-02	BE94991.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
676	5701	10709	3.86	7.3E-02	AE001789.1	NT	Thermotoga maritima section 101 of 136 of the complete genome
1450	7748	11508	2.33	7.3E-02	AW900281.1	EST_HUMAN	GM0-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1808	7766		11.5	7.3E-02	AL183302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4838	9822		1.14	7.3E-02	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
120	5190	10202	1.2	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039834 (section 88 of 148) of the complete genome
120	5190	10203	1.2	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039834 (section 88 of 148) of the complete genome
1446	6443	11501	1.87	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1446	6443	11502	1.87	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2478	7447		1.86	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 28 reverse transcriptase (pol) gene, internal fragment, partial cds
3761	8784	13799	1.82	7.2E-02	AW288322.1	EST_HUMAN	UI-H-BW0-ejl-a-05-Q-UJ.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732049 3'
4220	9213	14192	5.17	7.2E-02	BF572307.1	EST_HUMAN	60207775F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
1863	6852	11940	1.68	7.1E-02	L02280.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2225	7202		1.06	7.1E-02	AE004890.1	NT	Pseudomonas aeruginosa PA01, section 451 of 528 of the complete genome
2230	7207	12322	5.78	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092881 5'
4987	9969	14946	1.09	7.1E-02	BE208576.1	EST_HUMAN	ba10b05.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823921 5' similar to gb:X52851_rna1 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN); gb:X62803 Mouse mRNA for cyclophilin (MOUSE);
524	5559	10582	1.16	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1470	8467		0.92	7.0E-02	X98677.1	NT	M.arteilla Mcut-1 gene
1724	6719	11797	1.17	7.0E-02	AA056343.1	EST_HUMAN	z166104.s1 Strategene colon (#937204) Homo sapiens cDNA clone IMAGE:508599 3'
2860	7979	12893	2.25	7.0E-02	AW138152.1	EST_HUMAN	UI-H-B11-acy-c-07-Q-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
3802	8805	13810	0.82	7.0E-02	AA815438.1	EST_HUMAN	ai65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375878 3' similar to gb:K030002 60S
3931	8931	13922	1.07	7.0E-02	BE070284.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4017	8013		0.96	7.0E-02	AW782962.1	EST_HUMAN	QV4-B10407-280100-090-e10 BT0407 Homo sapiens cDNA
4093	9087	14078	1.2	7.0E-02	AF077821.1	NT	CM0-UM0001-080300-270-e12 UM0001 Homo sapiens cDNA
4773	9757	14745	7.8	7.0E-02	BF381987.1	EST_HUMAN	Caris familiaris inducible nitric oxide synthase mRNA, complete cds
510	5545	10548	17.58	6.9E-02	AL163210.2	NT	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
510	5545	10549	17.58	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1313	6310		1.29	6.8E-02	4507968	NT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3703	8707	13709	1.03	6.8E-02	Q06384	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)

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Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3703	8707	13710	1.03	6.8E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
1843	8833	11920	1.06	6.8E-02	AA496759.1	EST_HUMAN	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1843	8833	11921	1.06	6.8E-02	AA496759.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1865	8854	11942	3.07	6.8E-02	AF156673.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
3027	8044	13053	1.01	6.8E-02	AA781996.1	EST_HUMAN	Homo sapiens putative hepatic transcription factor (WBSCR14) gene, complete cds
3027	8044	13054	1.01	6.8E-02	AA781996.1	EST_HUMAN	ae30f02.r1 Soares testis NHT Homo sapiens cDNA clone 1376628 3'
3027	8044	13055	1.01	6.8E-02	AA781996.1	EST_HUMAN	al75a06.s1 Soares testis NHT Homo sapiens cDNA clone 1376628 3'
1497	6495		1.66	6.7E-02	AF115536.1	NT	al75a06.s1 Soares testis NHT Homo sapiens cDNA clone 1376628 3'
1854	6843	11831	1.32	6.7E-02	AI220285.1	EST_HUMAN	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds
3635	8841	13646	4.56	6.7E-02	P17278	SWISSPROT	qg79a04.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841408 3'
1330	6328	11376	1.14	6.6E-02	AI735509.1	EST_HUMAN	HOMEBOX PROTEIN HOXD4 (CHOX-A)
1352	6349	11399	0.98	6.6E-02	AF245116.1	NT	at12e09.x1 Baresteed aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2354920 3' similar to SW:LN1_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. ;
2117	7097	12210	1.74	6.6E-02	AJ289241.1	NT	Drosophila melanogaster cactin mRNA, complete cds
3382	8390	13413	9.7	6.6E-02	R64306.1	EST_HUMAN	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3398	8406	13432	2.63	6.6E-02	7108357	NT	y18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'
3398	8406	13433	2.63	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3985	8963	13953	1.53	6.6E-02	AF260225.1	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4819	9803	14783	9.95	6.6E-02	Q61703	SWISSPROT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
4819	9803	14784	9.95	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
577	5609	10608	2	6.5E-02	BF027639.1	EST_HUMAN	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
972	5988	11022	3.15	6.5E-02	7706068	NT	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
1368	6385	11414	2.48	6.5E-02	U47624.1	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1697	6692	11768	1.65	6.5E-02	AE000794.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
570	5603	10601	1.52	6.4E-02	X94549.1	NT	Aquifex aeolicus section 86 of 109 of the complete genome
1695	6690	11765	0.96	6.4E-02	AE001777.1	NT	A. carterae precursor of peridinin-chlorophyll-a-protein (PCP) gene
1695	6690	11766	0.96	6.4E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
2946	7895	12984	1.88	6.4E-02	6996923	NT	Thermotoga maritima section 89 of 136 of the complete genome
4928	8905	14883	1.21	6.4E-02	AL163247.2	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA
							Homo sapiens chromosome 21 segment HS21C047
1716	6711	11788	2.39	6.3E-02	AF108905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3523	8530		2.55	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
4129	9124	14108	3.54	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4212	9205		1	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4450	9440		5.96	6.2E-02	Q62191	SWISSPROT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO552)
5016	9987	14963	1.58	6.2E-02	RS9526.1	EST_HUMAN	y97a12.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41477 3' similar to gb:X57198_cds1
254	5314	10324	3.36	6.1E-02	D16471.1	NT	TRANSCRIPTION ELONGATION FACTOR S-II (HUMAN);
3885	8886		2.17	6.1E-02	U73325.1	NT	Human mRNA, Xq terminal portion
5000	9971	14947	0.92	6.1E-02	Y12503.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKK1) gene, complete cds
5018	9989		1.37	6.1E-02	A1220330.1	EST_HUMAN	S. scrofa mRNA for Man9-mannosidase
1243	6241	11282	0.88	6.0E-02	AE001777.1	NT	qg90e08.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1842470 3'
2700	7657		2.19	6.0E-02	AB031289.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
2866	5173	10183	0.91	6.0E-02	AA188730.1	EST_HUMAN	Mesocostoides corti mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2866	5173	10184	0.91	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
3158	8174	13186	1.82	6.0E-02	AA372376.1	EST_HUMAN	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
3158	8174	13197	1.62	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3549	8556		2.87	6.0E-02	BE984443.2	EST_HUMAN	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
229	5292	10300	6.97	5.9E-02	AW934719.1	EST_HUMAN	601658150R1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3876060 3'
2914	7933	12952	2.79	5.9E-02	AF190299.1	NT	RC1-DT0001-290100-012-010 DT0001 Homo sapiens cDNA
920	5936		3.97	5.8E-02	D90110.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
1620	6617	11683	2.52	5.8E-02	Q61768	SWISSPROT	Thiobacillus ferrooxidans merC, merA genes and URF-1
2789	7810		0.94	5.8E-02	AJ223621.1	NT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
3579	8586	13591	1.8	5.8E-02	AE001775.1	NT	Populus trichocarpa CCoAOMT1 gene, exon 1 to exon 5
4229	9223	14204	5.55	5.8E-02	AW051927.1	EST_HUMAN	Thermotoga maritima section 87 of 136 of the complete genome
4229	9223	14205	5.55	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4416	9408	14392	4.67	5.8E-02	A1247505.1	EST_HUMAN	wx24c02.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4416	9408	14393	4.67	5.8E-02	A1247505.1	EST_HUMAN	q15601.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:U13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4441	9431		2.28	5.8E-02	AF096284.1	NT	q15601.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:U13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4892	8964	14942	4.11	5.8E-02	7657006	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
							Homo sapiens dual adaptor of phosphotyrosine and 3-phosphoinositides (DAPPI), mRNA

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2983	8001	13013	1.08	5.7E-02	A081844.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP-C37A2.2
2998	8018	13028	1.11	5.7E-02	AF119117.1	NT	CE08611.1
3625	8632		1.02	5.7E-02	AF001292.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3712	8718	13718	2.21	5.7E-02	AW966791.1	EST_HUMAN	Chironomus thummi thummi globin VIIA.1 (ctt-7A.1), globin 8.1 (ctt-8.1), globin II-beta (ctt-2beta), non-functional globin XIII (ctt-13RT), globin XII (ctt-12) and globin XI (ctt-11) genes, complete cds
4546	8535		1.05	5.7E-02	M95089.1	NT	EST1378865 IMAGE resequences, MAGI Homo sapiens cDNA
1495	8493	11548	1.7	5.6E-02	AF094455.1	NT	Bos taurus lysozyme gene (cow 3), complete cds
2228	7203		1.01	5.6E-02	BE904308.1	EST_HUMAN	Hydrocotyle rotundifolia ribosomal protein L16 (rpl16) gene, intron; chloroplast gene for chloroplast product
4508	8498	14474	1.56	5.6E-02	AB013100.1	NT	601494578F2 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898610 5'
4557	8545	14530	0.84	5.6E-02	AA280599.1	EST_HUMAN	Lycopersicon esculentum LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
2583	7546	12660	4.77	6.5E-02	X97869.1	NT	z445c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3'
3143	8159	13181	3.85	5.5E-02		NT	H. sapiens gene encoding La autoantigen
4095	8089	14077	1.04	5.5E-02	L41561.1	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
1270	8288		0.75	5.4E-02	AF157623.1	NT	Gallid herpesvirus mRNA fragment
2953	7972		0.83	5.4E-02	AJ277468.1	NT	Homo sapiens HTA serine protease (PRSS11) gene, complete cds
3337	10056		6.65	5.4E-02	BE073468.1	EST_HUMAN	Oryza sativa rbb3-1 gene for putative Bowman Birik trypsin inhibitor
1036	6046	11075	1.48	5.3E-02	AW391248.1	EST_HUMAN	RC5-BT0569-140200-012-C03 BT0569 Homo sapiens cDNA
1036	6046	11076	1.48	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-409 ST0213 Homo sapiens cDNA
1476	6473	11531	7.24	5.3E-02	T94759.1	EST_HUMAN	QV0-ST0213-021299-062-409 ST0213 Homo sapiens cDNA
2424	7395	12518	1.9	5.3E-02	AJ276408.1	NT	vs37f12.1 Strategene lung (#937210) Homo sapiens cDNA clone IMAGE:119951 5' similar to gb:K01508
2872	7891	12913	0.82	5.3E-02	M58417.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2872	7891	12914	0.82	5.3E-02	M58417.1	NT	Pseudomonas putida tfgS gene
3079	8095	13109	4.71	5.3E-02	AJ276408.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
4916	8894	14868	9.18	5.3E-02	M80463.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
2221	7188		66.99	5.2E-02		NT	Pseudomonas putida tfgS gene
3040	8057	13065	2.21	5.2E-02	AJ277681.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
3040	8057	13068	2.21	5.2E-02	AJ277681.1	NT	Homo sapiens meprin A, alpha (PABA, peptide hydrolase) (MEP1A) mRNA
4166	9151	14133	3.13	5.2E-02	U07132.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
2303	7278		0.96	5.1E-02	AL134071.1	EST_HUMAN	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4845	9827		0.91	5.1E-02	AB031740.1	NT	Human steroid hormone receptor Nr-1 mRNA, complete cds
							DKFZp547D073_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D073 5'
							Homo sapiens PBI gene for salivary proline-rich protein P-B, complete cds

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
479	5518	10526	1.87	5.0E-02	AF098004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1185	6186	11223	12.26	5.0E-02	Z99104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
1944	6930	12029	2.86	5.0E-02	P02810	SWISSPROT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-F/PIF-S) (PROTEIN APROTEIN C) [CONTAINS: PEPTIDE P-C]
2746	6987	11021	1.3	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3263	8276		1.24	5.0E-02	7305610	NT	Mus musculus Uuc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3515	8523		1.04	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3600	8607	13615	7.08	5.0E-02	U12769.2	NT	Antheraea pernyi period clock protein homolog mRNA, complete cds
223	5285		30.11	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
368	5417	10431	2.47	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
368	5417	10432	2.47	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
2803	7623	12838	0.89	4.8E-02	U32636.1	NT	Zea mays phytoene synthase (Y1) gene, complete cds
3217	8232	13253	1.52	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN)
3490	8498		2.64	4.9E-02	AA188940.1	EST_HUMAN	zq48a12.s1 Stragene NNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632928 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element
3511	8519	13530	0.71	4.9E-02	AA400914.1	EST_HUMAN	z178a03.s1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:728428 3'
3511	8519	13531	0.71	4.9E-02	AA400914.1	EST_HUMAN	z178a03.s1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:728428 3'
4892	9877	14680	2.02	4.9E-02	AW187821.1	EST_HUMAN	xg56g10.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2632386 3'
4892	9877	14681	2.02	4.9E-02	AW187821.1	EST_HUMAN	xg56g10.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2632386 3'
328	5381	10390	1.13	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
329	5381	10390	2.65	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
485	5522	10531	8.84	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2211	7188	12309	1.27	4.8E-02	W51983.1	EST_HUMAN	z049b02.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P88 (HUMAN);
3136	8162	13175	2.05	4.8E-02	X17144.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
268	5327	10338	1.22	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
730	5753	10774	2.88	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1855 section 335 of 400 of the complete genome
1273	6271		0.71	4.6E-02	A014255.1	EST_HUMAN	am50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TR:P80533
1342	6339	11390	2.41	4.6E-02	AV727059.1	EST_HUMAN	P90533 LIMA :contains element LTR1 repetitive element
2418	7389	12509	2.09	4.6E-02	AW236023.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HTCBW C01 5'
2736	5327	10338	2.36	4.6E-02	BE153583.1	EST_HUMAN	xn24f03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694653 3' similar to SW:GRF1_HUMAN
3416	7958	12976	0.76	4.6E-02	BE153583.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1
							PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
							PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4004	9000		0.86	4.6E-02	AF220365.1	NT	Mus musculus nuclear RNA helicase II/Gu (dbs21) gene, complete cds
444	5481	10499	1.67	4.5E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1199	6200	11236	0.81	4.5E-02	AF005730.1	NT	Marburg virus strain M5.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1199	6200	11237	0.81	4.5E-02	AF005730.1	NT	Marburg virus strain M5.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1768	6760	11847	4.15	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2051	7033	12145	2.17	4.5E-02	AE003964.1	NT	Xylella fastidiosa, section 110 of 229 of the complete genome
3640	8646	13653	3.82	4.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
219	5282		3.85	4.4E-02	BE927273.1	EST_HUMAN	601652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5'
2039	7022		3.33	4.4E-02	P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2419	7380	12510	1.11	4.4E-02	AW875475.1	EST_HUMAN	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
3555	8562	13568	1.81	4.4E-02	AF159160.1	NT	Myxococcus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4493	9483	14461	0.99	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4483	9483	14462	0.99	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
772	5794	10822	6.82	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
3345	8354	13372	8.44	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3575	8582		1.23	4.3E-02	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
812	5833	10866	1.73	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
855	5874		1.9	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
885	5903	10944	1.49	4.2E-02	AW003645.1	EST_HUMAN	w34g01.x1 NCI_CGAP_P111 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291
1682	6878		2.39	4.2E-02	AL445066.1	NT	L1 RETROPOSON, ORF2 MRNA, contains L1.13 L1 L1 repetitive element ;
3580	8587	13592	1.51	4.2E-02	P23091	SWISSPROT	Thermoplasma acidophilum complete genome; segment 4/5
4600	9588	14576	3.38	4.2E-02	BF342995.1	EST_HUMAN	TRANSFORMING PROTEIN MAF
2605	7567	12682	1.08	4.1E-02	AE002330.2	NT	602017105F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4152672 5'
4347	9336		8.04	4.1E-02	AW893484.1	EST_HUMAN	Chlamydia muridarum, section 60 of 85 of the complete genome
4954	9931		0.87	4.1E-02	X85980.1	NT	QV1-NN0012-180400-164-06 NN0012 Homo sapiens cDNA
1603	6599	11660	0.9	4.0E-02	AI675992.1	EST_HUMAN	L monocytogenes type 3 partial lap gene (strain 443)
3170	8186	13207	3.01	4.0E-02	AB040904.1	NT	wb98h01.x1 NCI_CGAP_P228 Homo sapiens cDNA clone IMAGE:2313745 3'
1103	6110	11141	3.41	3.9E-02	BF516149.1	EST_HUMAN	Homo sapiens mRNA for KIAA1471 protein, partial cds
1326	6324	11371	1.9	3.9E-02	P41047	SWISSPROT	UI-H-BW1-anx-h-08-Q.U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1921	6907	12001	1.85	3.9E-02	AJ403386.1	NT	FAS ANTIGEN LIGAND
							M.musculus DNA for desmin-binding fragment DesiD7

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2632	7692		1.51	3.9E-02	4506862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
977	5992	11025	5.31	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
2175	7154	12274	5.07	3.7E-02	A1984806.1	EST_HUMAN	wr85608.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
2502	7470	12586	1.04	3.7E-02	AB018261.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
2976	7894	13008	1.04	3.7E-02	P76944	SWISSPROT	ECM3/ODERM1
2978	7896	13009	3.76	3.7E-02	BF312863.1	EST_HUMAN	601806233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5'
3372	8380		1.16	3.7E-02	6880541	NT	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnma3), mRNA
3115	8131	13150	43.98	3.6E-02	AP000003.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 544001-777000 nt position (3/7)
3670	8577	13583	0.8	3.6E-02	KT3221.1	NT	H. vulgare Ss1 gene for sucrose synthase
3578	8585	13590	0.73	3.6E-02	AL098806.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
884	5902	10943	1.6	3.5E-02	U09506.1	NT	Drosophila melanogaster tiggerin mRNA, complete cds
993	6006	11037	1.11	3.5E-02	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1531	6529	11588	1.01	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1531	6529	11589	1.01	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4092	9086	14075	3.28	3.5E-02	AE001773.1	NT	Thermoloba maritima section 85 of 136 of the complete genome
4189	9182	14165	1.13	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
573	5606	10604	1.18	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
573	5606	10605	1.18	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
574	5606	10604	4.61	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
574	5606	10605	4.61	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1034	6044	11073	3.13	3.4E-02	AW274020.1	EST_HUMAN	xv28d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW:C211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
1187	6188		9.31	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2328	7302	12422	1.86	3.4E-02	T67160.1	EST_HUMAN	yc20d06.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element
3346	8355	13373	1.39	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3688	8692	13694	0.7	3.4E-02	BE639514.1	EST_HUMAN	RC3-FN0155-060700-011-d10 FN0155 Homo sapiens cDNA
3821	8823	13830	3.3	3.4E-02	AW784952.1	EST_HUMAN	RC6-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4467	9457	14437	3.07	3.4E-02	X59799.1	NT	M.musculus S-antigen gene promoter region
4892	9871		2.79	3.4E-02	Q26457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4909	9885	14856	1.61	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
371	5420		15.92	3.3E-02	AA398735.1	EST_HUMAN	z75e08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1149	6163	11185	14.2	3.3E-02	AB035867.1	NT	Cricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1599	6595	11656	1.34	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2031	7014		1.55	3.3E-02	R09112.1	EST_HUMAN	y25c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
4053	6595	11656	2.72	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4343	9334	14318	2.08	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp96 (Tra1), mRNA
132	5196	10214	2.52	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1109	6115	11145	14.14	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1109	6115	11146	14.14	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
2060	7042		8.6	3.2E-02	P28955	SWISSPROT	LARGE TEGUMENT PROTEIN
3061	8078	13091	13.22	3.2E-02	BE867353.1	EST_HUMAN	601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'
3832	8638	13644	1.3	3.2E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
3854	8856	13861	0.88	3.2E-02	Z74103.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL055c
3854	8856	13862	0.88	3.2E-02	Z74103.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL055c
4097	9091		17.68	3.2E-02	X94768.1	NT	H.sapiens RP3 gene (XLRP gene 3)
4622	9607	14595	3.39	3.2E-02	AF114182.1	NT	Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
4881	9666	14648	2.57	3.2E-02	AF067083.1	NT	Vitreoscilla sp. outer membrane protein homolog gene, complete cds; Ttp repressor binding protein gene, partial cds; and unknown genes
1241	6239		1.62	3.1E-02	4503416	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1286	6285	11328	1.44	3.1E-02	P18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1852	6841	11929	0.95	3.1E-02	6671564	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
4998	9117		12.58	3.1E-02	AU119008.1	EST_HUMAN	AU119008 HEMBA1 Homo sapiens cDNA clone HEMBA1004842 5'
5072	10041		5.51	3.1E-02	5730074	NT	Homo sapiens fibrinogen-like 2 (FGL2), mRNA
1584	6581		11.29	3.0E-02	AF187125.1	NT	Pityokines minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
2509	7477	12592	0.99	3.0E-02	AA402242.1	EST_HUMAN	z65h03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727253 5'
3486	8494	13511	0.95	3.0E-02	M94176.1	NT	Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds
3569	8576	13582	2.92	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3660	8665		0.72	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0296-150200-040-e09 ST0296 Homo sapiens cDNA
4885	9884	14834	7.12	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4885	9884	14835	7.12	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2368	7769	12459	1.06	2.9E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
3827	8829	13838	1.37	2.9E-02	H72805.1	EST_HUMAN	y07e10.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:233130 5'
3877	8878	13881	0.73	2.9E-02	O15440	SWISSPROT	MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 5 (ABC TRANSPORTER MOAT-C) (PABC11) (SMRP)
4858	9839	14812	1.81	2.9E-02	X65137.1	NT	S. vulgaris pepC gene for PEP carboxylase
4858	9839	14813	1.81	2.9E-02	X65137.1	NT	S. vulgaris pepC gene for PEP carboxylase
2408	7377		1	2.8E-02	AA782516.1	EST_HUMAN	al55c09.s1 Soares parathyroid tumor 2NHPA Homo sapiens cDNA clone 1360912 3'
3286	8297	13323	1.1	2.8E-02	AF066083.1	NT	Homo sapiens retinal fasciclin (FSCN2) gene, exon 2
3286	8297	13324	1.1	2.8E-02	AF066083.1	NT	Homo sapiens retinal fasciclin (FSCN2) gene, exon 2
4185	9178		0.8	2.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Map1), mRNA
1457	6454	11513	1.09	2.7E-02	U66059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2P, TCRBV7S2A1N4T, TCRBV13S9/13S>
3347	8356	13374	1.84	2.7E-02	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4079	9073	14060	2.12	2.7E-02	N47258.1	EST_HUMAN	yy66h12.r1 Soares multiple sclerosis 2NBMSP Homo sapiens cDNA clone IMAGE:280487 5'
4079	9073	14081	2.12	2.7E-02	N47258.1	EST_HUMAN	yy66h12.r1 Soares multiple sclerosis 2NBMSP Homo sapiens cDNA clone IMAGE:280487 5'
5040	10011	14980	1.04	2.7E-02	T85073.1	EST_HUMAN	ys39f04.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:120127 3' similar to contains Alu repetitive element
566	5599	10598	0.98	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1350	6347		0.83	2.6E-02	AW850515.1	EST_HUMAN	IL3-CT0219-280100-082-C09 CT0219 Homo sapiens cDNA
2305	7280	12398	1.97	2.6E-02	AA490021.1	EST_HUMAN	ab02502.s1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2307	7282	12400	1.99	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2307	7282	12401	1.99	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2845	7865		1.39	2.6E-02	AF109906.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70
4749	9734	14720	3.57	2.6E-02	L12032.1	NT	and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes
4759	9743	14728	1.27	2.6E-02	AJ403239.1	NT	Chicken dorsalin-1 mRNA, complete cds
4759	9743	14729	1.27	2.6E-02	AJ403239.1	NT	M. musculus DNA for vimentin-binding fragment VintE7
4897	9876	14844	1.74	2.6E-02	AE002014.1	NT	M. musculus DNA for vimentin-binding fragment VintE7
4921	9899	14874	2.61	2.6E-02	AW241154.1	EST_HUMAN	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1
528	5563	10568	1.4	2.6E-02	A1783130.1	EST_HUMAN	xa52b04.x1 NCI CGAP Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN Q15041 HYPOTHETICAL PROTEIN KIAA0069 ; on28f06.y6 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
528	5563	10567	1.4	2.5E-02	AI793130.1	EST_HUMAN	on26f06.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
800	5821	10851	12.78	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950685 3'
858	6077	10918	4.21	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950685 3'
2689	7647		1.83	2.6E-02	U12571.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
2885	7904	12924	3.25	2.5E-02	X98697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
2885	7904	12925	3.25	2.5E-02	X98697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
3932	10049	13923	0.85	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
3932	10049	13924	0.85	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4083	9077	14085	5.51	2.5E-02	AW592114.1	EST_HUMAN	h36h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2634015 3'
173	5237	10249	0.68	2.4E-02	AW592114.1	EST_HUMAN	h36h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2070156 3'
1563	6560	11622	1.88	2.4E-02	H65884.1	EST_HUMAN	h75f11.1 Soares_fetal_liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211149 5'
1993	7760	12082	1.31	2.4E-02	P01801	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
1993	7760	12083	1.31	2.4E-02	P01801	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4243	9237	14220	1.46	2.4E-02	J05110.1	NT	T. thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4390	9381	14392	1.56	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4390	9381	14393	1.56	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
1834	6824		3.68	2.3E-02	W05340.1	EST_HUMAN	za84g08.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:289284 5'
1848	6837		5.18	2.3E-02	U94185.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2289	7264	12382	1.88	2.3E-02	Z74289.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c
3588	8605	13613	5.37	2.3E-02	Z20377.1	EST_HUMAN	HSAAACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA
4026	9022	14009	0.76	2.3E-02	L24789.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4026	9022	14010	0.76	2.3E-02	L24789.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4296	9288	14275	1.14	2.3E-02	AW889107.1	EST_HUMAN	CM4-NN0080-290400-160-b04 NN0080 Homo sapiens cDNA
4327	9319	14301	0.85	2.3E-02	BE952225.1	EST_HUMAN	CM3-MT0118-010800-318-g07 MT0118 Homo sapiens cDNA
4327	9319	14302	0.85	2.3E-02	BE952225.1	EST_HUMAN	CM3-MT0118-010800-318-g07 MT0118 Homo sapiens cDNA
4328	10051	14303	0.82	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770871 3'
4328	10051	14304	0.82	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770871 3'
4463	9453	14434	2.76	2.3E-02	BF026487.1	EST_HUMAN	60167278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4463	9453	14435	2.76	2.3E-02	BF026487.1	EST_HUMAN	60167278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4860	9841		0.95	2.3E-02	7682173	NT	Homo sapiens KIAA0547 gene product (KIAA0547), mRNA
4977	9953	14931	0.77	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
4977	9953	14932	0.77	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
728	5751	10772	2.95	2.2E-02	AF018267.1	NT	Columba livia nucleoside diphosphate kinase (NDFK) gene, nuclear gene encoding mitochondrial protein, complete cds

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Table 4
Single Exon Probes Expressed in HBL100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1708	6703		1.21	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
1723	6718	11785	0.97	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1723	6718	11798	0.97	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1965	6950	12053	1.43	2.2E-02	282001.1	NT	S.pneumoniae pcpA gene and open reading frames
3350	8369		1.88	2.2E-02	AA577785.1	EST_HUMAN	nm24a04.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3561	8588		3.57	2.2E-02	AF093094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3763	8766	13769	1.18	2.2E-02	AW601317.1	EST_HUMAN	PMO-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA
3820	8822	13829	0.68	2.2E-02	Z74283.1	NT	S.cerevisiae chromosome IV reading frame ORF YJL245c
416	5453		4.33	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
448	5483		7.77	2.1E-02	AF029726.1	NT	Dictyostellum discoideum histidine kinase C (dhkC)mRNA, complete cds
							Bacillus subtilis cotKLM cluster, CotK (cotK), CotL (cotL), and spore coat protein CotM (cotM) genes, complete cds
1244	6242	11283	7.23	2.1E-02	U72073.1	NT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1744	6739	11816	1.17	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1744	6739	11817	1.17	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1744	6739	11818	1.17	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
2744	5792	10820	3.7	2.1E-02	N29266.1	EST_HUMAN	y43h07.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:284541 5'
3502	8510	13524	0.84	2.1E-02	AA491271.1	EST_HUMAN	z63b09.r1 Soares_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796121 5'
4009	8005	13993	0.67	2.1E-02	Z74283.1	NT	S.cerevisiae chromosome IV reading frame ORF YJL245c
4182	9175	14169	0.8	2.1E-02	BF343955.1	EST_HUMAN	602015306F1 NCL_CGAP_Bm94 Homo sapiens cDNA clone IMAGE:4151161 5'
4322	9314	14297	1.92	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
4333	9324	14310	1.35	2.1E-02	AI768127.1	EST_HUMAN	wg91d11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4540	9356		0.68	2.1E-02	Y19213.1	NT	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7
4572	9560	14549	6.38	2.1E-02	Y08501.1	NT	A.thaliana mitochondrial genome, part A
4591	9579	14569	0.76	2.1E-02	AA665737.1	EST_HUMAN	eg55g12.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'
17	5097	10080	1.78	2.0E-02	BF002932.1	EST_HUMAN	7g51c08.x1 NCL_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.13
18	5098	10081	9.9	2.0E-02	AW895565.1	EST_HUMAN	MER1 repetitive element
257	5317	10326	2.81	2.0E-02	6753635	NT	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
283	5350	10363	1.85	2.0E-02	AA456538.1	EST_HUMAN	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
780	5811	10841	1.4	2.0E-02	6753635	NT	eat15b10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
							Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
							Homo sapiens genomic region containing hypervariable minisatellites chromosome 1[1p36.33] of Homo sapiens
1071	6079	11110	1	2.0E-02	AL098805.1	NT	sapiens
1180	6182	11219	1.31	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FL10379 (FL10379), mRNA
1180	6182	11220	1.31	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FL10379 (FL10379), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1835	6825	11912	1.69	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1835	6825	11913	1.69	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2726	7683		1.8	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3005	5097	10080	1.66	2.0E-02	BF002932.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:330998 3' similar to contains MER1.13
3071	8087		2.21	2.0E-02	7305474	NT	MER1 repetitive element ; Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6b), mRNA
3156	8172		1.54	2.0E-02	AF095588.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
3900	8900	13698	1.61	2.0E-02	M18095.1	NT	P.vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
4943	9820		0.84	2.0E-02	AI271895.1	EST_HUMAN	q83603.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1866076 3'
684	5708	10720	1.76	1.9E-02	AA572764.1	EST_HUMAN	nf19a07.s1 NCI_CGAP_Pt1 Homo sapiens cDNA clone IMAGE:914198 similar to contains L1.11 L1 repetitive element ;
1988	6973	12077	2.16	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
1988	6973	12078	2.16	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2434	7405	12523	1.18	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2835	7655	12874	7.79	1.9E-02	AA713958.1	EST_HUMAN	nw04f05.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3'
2881	7900	12922	1.67	1.9E-02	AV648669.1	EST_HUMAN	AY648669 GLC Homo sapiens cDNA clone GLCBLH07 3'
3185	8201		0.75	1.9E-02	AB033811.1	NT	Utrichus talpoides mitochondrial gene for cytochrome b, complete cds
3530	8536		0.91	1.9E-02	N52250.1	EST_HUMAN	y228b02.s1 Soares_multiple_sclerosis_2NBMSP Homo sapiens cDNA clone IMAGE:284331 3'
3622	8629		8.78	1.9E-02	BE738088.1	EST_HUMAN	601672862F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5'
3633	8639	13645	0.74	1.9E-02	AI301183.1	EST_HUMAN	q04c07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element ;
3834	8933	13926	1.5	1.9E-02	AF141940.1	NT	Mycoplasma imitans VhaA1 precursor (vhaA1) and VhaA2 precursor (vhaA2) genes, partial cds
4070	9084	14053	1.75	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4070	9084	14054	1.75	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4410	9400	14385	2.81	1.9E-02	AI452989.1	EST_HUMAN	h46d04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element ;
4852	7405	12523	3.15	1.9E-02	AL161550.2	NT	contains Alu repetitive element ;
344	5396	10403	1.36	1.8E-02	AW771104.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
1142	6146	11178	1.42	1.8E-02	X17664.1	NT	hm52c08.x1 NCI_CGAP_Cot7 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element
2607	7569	12884	1.45	1.8E-02	AE004544.1	NT	MER29 repetitive element ;
3138	8154		0.59	1.8E-02	AI805828.1	EST_HUMAN	H.francisci mRNA for myelin basic protein (MBP)
3793	8766	13801	0.91	1.8E-02	AW879122.1	EST_HUMAN	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
							h652a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296 3'
							MR1-OT0011-280300-008-g04 OT0011 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3793	8796	13802	0.91	1.8E-02	AW878122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3970	8969		1.08	1.8E-02	AA861448.1	EST_HUMAN	ak24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406935 3'
4308	9298	14284	1.59	1.8E-02	AW936363.1	EST_HUMAN	QV4-DT0021-301289-071-b11 DT0021 Homo sapiens cDNA
4798	9782	14765	0.95	1.8E-02	O60810	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.2
895	5913	10952	1.21	1.7E-02	BE394869.1	EST_HUMAN	601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632180 5'
1753	6747	11828	2.15	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.1 L1 repetitive element;
1753	6747	11829	2.15	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.1 L1 repetitive element;
1833	6823		2.15	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2054	7038		7.25	1.7E-02	AB004818.1	NT	Oryctolagus cuniculus mRNA for mitogenin29, complete cds
2569	7532		1.47	1.7E-02	7657495	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
2929	7948	12966	1.09	1.7E-02	AI147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
3433	8441		4.78	1.7E-02	AW827388.1	EST_HUMAN	hm45a04.x1 NCJ_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element;
4045	9041		1.04	1.7E-02	AA669618.1	EST_HUMAN	ac19f04.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
4071	8071		1.86	1.7E-02	R02508.1	EST_HUMAN	ye86f08.r1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124647 5'
4332	9323	14309	1.34	1.7E-02	AI305279.1	EST_HUMAN	qm08g07.x1 NCJ_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881278 3' similar to gb:X52359 ZINC FINGER PROTEIN 30 (HUMAN);
4396	9387	14370	1.47	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.1 L1 repetitive element;
4576	9584	14552	1.82	1.7E-02	V00641.1	NT	Messenger RNA for anglerfish (Lophius americanus) somatostatin II
4698	9653		8.98	1.7E-02	AI015076.1	EST_HUMAN	ov51e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
507	5542		1.83	1.6E-02	AL021928.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
1616	6613	11680	1.13	1.6E-02	Y18889.1	NT	Treponema maltophilum flaB2, flaB3 and flilD genes; for flagellin subunit proteins and CAP protein homologue
2187	7166	12285	1.01	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2187	7166	12286	1.01	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2572	7535	12652	1.12	1.6E-02	AA484872.1	EST_HUMAN	ne81d06.s1 NCJ_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910567
2622	7584		0.95	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
2951	7970	12987	0.73	1.6E-02	AF112282.1	NT	Lasaea sp. isolate Ibd cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product
3447	8455	13481	5.11	1.6E-02	AW850552.1	EST_HUMAN	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3758	8761	13761	1.1	1.6E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
4051	9047		1.82	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RelGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
742	5765		23.96	1.5E-02	8923734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2081	7062	12171	2.42	1.5E-02	N39521.1	EST_HUMAN	w27b07.s1 Soares fetal liver spleen TNF1LS Homo sapiens cDNA clone IMAGE:243925 3'
2110	7090	12204	1.29	1.5E-02	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
2887	8005	13017	1.24	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
2887	8005	13018	1.24	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3641	8847	13654	0.88	1.5E-02	BF092942.1	EST_HUMAN	MR4-TN0115-080900-201-b72 TN0115 Homo sapiens cDNA
5006	9977	14952	0.97	1.5E-02	4503534	NT	Homo sapiens eukaryotic translation initiation factor 4E (EIF4E) mRNA
414	5451		1.25	1.4E-02	AE002230.2	NT	Chlamydomonas reinhardtii AR39, section 58 of 64 of the complete genome
1101	6108	11138	3.55	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC51225), mRNA
1237	6235		1.37	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1279	6278		2.38	1.4E-02	U67778.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1486	6483		0.96	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAHH11 5'
2926	7945	12962	0.87	1.4E-02	7657040	NT	Homo sapiens down-regulated in metastasis (DRIM), mRNA
3140	8156	13177	2.22	1.4E-02	AF160969.2	NT	Bifidobacterium longum Na+/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (aglL) genes, complete cds; and N-acetylglucosamine/xylose repressor protein (nagC/xyR) gene, partial cds
3314	8325	13347	0.73	1.4E-02	AW074212.1	EST_HUMAN	x609409.xt NC1 CGAP GU1 Homo sapiens cDNA clone IMAGE:2575793 3'
3404	8413	13439	6.12	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3404	8413	13440	6.12	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3572	8579	13585	10.27	1.4E-02	6996918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4361	9352	14331	7.06	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGG resequences, MAGG Homo sapiens cDNA
4361	9352	14332	7.06	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGG resequences, MAGG Homo sapiens cDNA
4726	9711	14695	6.63	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4726	9711	14696	6.63	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
1828	6918		1.4	1.3E-02	BE739263.1	EST_HUMAN	601566462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826336 5'
1915	6901	11694	1.7	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2934	7953	12970	0.87	1.3E-02	M81725.1	NT	Oenothera lamarckiana NADH dehydrogenase subunit 2 (nad2) gene, exons 1-2
3141	8157	13178	1.9	1.3E-02	BF697081.1	EST_HUMAN	602128475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3141	8157	13179	1.9	1.3E-02	BF697081.1	EST_HUMAN	602128475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3662	8864		1.18	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4771	9755	14742	1.07	1.3E-02	U66081.1	NT	Human germ-line T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV16S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, z65g01.r1 Soares retina N2b4-HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element;
353	5404	10414	4.04	1.2E-02	AA059299.1	EST_HUMAN	
450	5487	10502	1.52	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION
729	5752	10773	5.89	1.2E-02	AI183522.1	EST_HUMAN	q68e12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.11 L1 repetitive element;
2112	7082	12208	1.27	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2116	7085	12209	1.07	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
2375	7347	12468	1.15	1.2E-02	AW172350.1	EST_HUMAN	x37c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2564	7347	12468	1.16	1.2E-02	AW172350.1	EST_HUMAN	x37c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3028	8045	13251	1.97	1.2E-02	AA076418.1	EST_HUMAN	zm86e03.r1 Stralagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545020 5'
3215	8230	13251	1.97	1.2E-02	R62805.1	EST_HUMAN	y11b08.st Soares placenta N2b4HP Homo sapiens cDNA clone IMAGE:138903 3'
4729	9714	14699	0.95	1.2E-02	6754387	NT	Mus musculus interferon regulatory factor 5 (Ifi5), mRNA
4761	9745	14731	3.66	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
4876	9855		1.51	1.2E-02	AB019786.1	NT	Cynops pyrrhogaster CpUbiq1 mRNA, partial cds
4912	9891	14865	2.45	1.2E-02	AB019786.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5025	9896	14969	1.29	1.2E-02	AF185576.1	NT	Mus musculus POZ/zinc finger transcription factor ZDA-8 mRNA, complete cds
1250	6248	11289	1.26	1.1E-02	AA070364.1	EST_HUMAN	zm69e11.st Stralagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530924 3'
1668	6684	11739	1.43	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1668	6684	11740	1.43	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1987	6972	12076	3.37	1.1E-02	BF345263.1	EST_HUMAN	602018037F1 NCL CGAP_Bn87 Homo sapiens cDNA clone IMAGE:4163808 5'
2808	7828		4.07	1.1E-02	N99523.1	EST_HUMAN	zm40e05.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:295040 5'
3444	8452	13476	3.11	1.1E-02	AI653508.1	EST_HUMAN	iq95b10.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XP_F_HUMAN
3980	8988		0.69	1.1E-02	AW813786.1	EST_HUMAN	Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL;
4683	9668	14650	2.3	1.1E-02	AL048383.2	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
7	5087	10073	8.28	1.0E-02	AW846120.1	EST_HUMAN	DKFZp586E0924_s1 586 Homo sapiens cDNA clone DKFZp586E0924
2497	7465		0.95	1.0E-02	AA806389.1	EST_HUMAN	MR3-CT01176-111099-003-e10 CT0176 Homo sapiens cDNA
3016	8033	13044	2.95	1.0E-02	BE835566.1	EST_HUMAN	cc22h08.st NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350495 3'
							RCO-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3188	8204	13228	0.98	1.0E-02	BE988999.1	EST_HUMAN	601849867R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'
4632	8617	14608	4.68	1.0E-02	6753521	NT	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
4697	9682	14665	3.4	1.0E-02	R06567.1	EST_HUMAN	yq54h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199633 5'
4855	9836	14810	1.72	1.0E-02	L05632.1	NT	Human glycoprotein hormone alpha-subunit (GCA) gene, 5' flank
882	5900	10941	2.15	9.0E-03	A1798126.1	EST_HUMAN	wh4209.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
1245	6243		1.46	9.0E-03	BE781889.1	EST_HUMAN	MER22 MER22 repetitive element ;
2331	7305	12425	1.79	9.0E-03	AL161559.2	NT	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'
4828	9812	14793	1.02	9.0E-03	BE047949.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
5026	9997	14970	0.98	9.0E-03	6753521	NT	tz44e10.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291466 5'
498	5534		2.78	8.0E-03	AA723007.1	EST_HUMAN	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
974	5990	11023	52.19	8.0E-03	AF106658.1	NT	zh30e03.s1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413596 3' similar to contains
2095	7076	12190	1.39	8.0E-03	AL163283.2	NT	Alu repetitive element;
3280	8292	13317	0.68	8.0E-03	AJ131016.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
3591	8598	13603	1.23	8.0E-03	P32844	SWISSPROT	Homo sapiens SCL gene locus
3591	8598	13604	1.23	8.0E-03	P32844	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4134	9129	14112	0.95	8.0E-03	BE840049.1	EST_HUMAN	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4258	9252	14239	5.95	8.0E-03	BF363327.1	EST_HUMAN	QV0-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA
685	5709	10721	11.47	7.0E-03	AF097183.1	NT	CM4-NN0119-300600-223-505 NN0119 Homo sapiens cDNA
685	5709	10722	11.47	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
962	5977	11011	11.8	7.0E-03	AF243376.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
1099	6106	11136	2.63	7.0E-03	AV731712.1	EST_HUMAN	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1372	6369	11418	2.08	7.0E-03	AA668298.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1473	6470	11528	4.65	7.0E-03	AW303599.1	EST_HUMAN	ab78b09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3'
2168	7765	12297	1.38	7.0E-03	P04929	SWISSPROT	xv21b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
3680	8695	13687	0.92	7.0E-03	AW444463.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3722	8726	13726	0.78	7.0E-03	AF196344.1	NT	UI-H-B13-alk-c-10-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4213	9206		1.05	7.0E-03	U60086.1	NT	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4404	9395		1.12	7.0E-03	AW117711.1	EST_HUMAN	Dicystostellum discoideum multidrug resistance transporter/Ser protease (tagC) mRNA, complete cds
4468	9458		1.1	7.0E-03	AW630888.1	EST_HUMAN	xe34f09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2609033 3' similar to TR:Q12987 Q12987
							ACIDIC 82 KDA PROTEIN. ;
							hh89e05.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969936 5'

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4830	8814		2.67	7.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
1221	6221	11263	9.46	6.0E-03	AW511148.1	EST_HUMAN	h22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810224 3' similar to SW:PXN_HUMAN O75469 ORPHAN NUCLEAR RECEPTOR PXR;
1221	6221	11264	9.46	6.0E-03	AW511148.1	EST_HUMAN	h22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810224 3' similar to SW:PXN_HUMAN O75469 ORPHAN NUCLEAR RECEPTOR PXR;
2699	7656	12770	1.02	6.0E-03	AF112374.1	NT	Danio rerio odorant receptor gene cluster
2820	7841	12857	4.18	6.0E-03	AA759135.1	EST_HUMAN	h78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
2820	7841	12858	4.18	6.0E-03	AA759135.1	EST_HUMAN	h78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
3173	8189		2.91	6.0E-03	HT5690.1	EST_HUMAN	y77h04.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:211351 5'
3232	8247		0.85	6.0E-03	AF190338.1	NT	Noturus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3298	8309	13335	1.31	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplerin reductase and vasolobin genes, complete cds
3298	8309	13336	1.31	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplerin reductase and vasolobin genes, complete cds
3470	8478		1.13	6.0E-03	W37885.1	EST_HUMAN	zc13a11.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3576	8583	13588	5.07	6.0E-03	BF510986.1	EST_HUMAN	UI-H-B14-apm-c-08-0-UJ.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3611	8618	13628	1.29	6.0E-03	BE077356.1	EST_HUMAN	RC1-BT0606-260400-014-a07 BT0606 Homo sapiens cDNA
3690	8694	13696	1.18	6.0E-03	6754028	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpi), mRNA
3850	8852		0.86	6.0E-03	BE250108.1	EST_HUMAN	600942904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959513 6'
4199	9192		1.31	6.0E-03	N58946.1	EST_HUMAN	y62h10.s1 Soares_multiple_sclerosis_2NbHMSPI Homo sapiens cDNA clone IMAGE:278179 3'
4239	9233		1.27	6.0E-03	AJ018633.1	EST_HUMAN	ov33c11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4556	9544	14529	6.94	6.0E-03	AA324242.1	EST_HUMAN	EST27116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
4650	8927		0.98	6.0E-03	L34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
561	5688	10696	1.81	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds, complete ORFA, and grpE-like protein, complete cds
561	5688	10697	1.81	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds, complete ORFA, and grpE-like protein, complete cds
662	5696	10696	2.2	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds, complete ORFA, and grpE-like protein, complete cds
662	5696	10697	2.2	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds, complete ORFA, and grpE-like protein, complete cds
1095	6102	11132	1.24	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
2610	7572	12888	2.3	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2865	7885	12905	0.69	5.0E-03	BE266057.1	EST_HUMAN	601194706F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538789 5'
3063	8080	13094	3.89	5.0E-03	T87623.1	EST_HUMAN	yc81109.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22395 3'
3081	8097		2.71	5.0E-03	AL181491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3093	8109	13128	1.36	5.0E-03	RL1794.1	EST_HUMAN	y86g02.s1 Soares breast 2N1bHst Homo sapiens cDNA clone IMAGE:155668 3'
3204	8219		0.75	5.0E-03	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3616	8623	13631	3.67	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (penB) gene, complete cds
3673	8678	13681	0.67	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
3864	8868		1.7	5.0E-03	AA298675.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4179	8678	13681	0.68	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4478	9466	14445	0.78	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
4580	9568	14557	1.55	5.0E-03	AJ752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC, cn15c02 random
232	5295	10304	2.13	4.0E-03	AW500196.1	EST_HUMAN	UI-HF-BN0-akc-h-04-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
319	5374	10383	1.88	4.0E-03	R46482.1	EST_HUMAN	y51e04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
440	5477	10485	0.87	4.0E-03	P54675	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (P13K)
598	5629	10628	3.1	4.0E-03	AA939339.1	EST_HUMAN	cn75g12.s1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1562568 3'
866	5884	10927	1.7	4.0E-03	R46482.1	EST_HUMAN	y51e04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
800	5918		2.96	4.0E-03	AW749101.1	EST_HUMAN	RC3-BT0333-110100-012-01 BT0333 Homo sapiens cDNA
1133	6138	11169	24.08	4.0E-03	AA099777.1	EST_HUMAN	Z81a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
1151	6155	11188	1.42	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1284	6283	11325	1.02	4.0E-03	AA284374.1	EST_HUMAN	zs59a01.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1551	6548		1.28	4.0E-03	AV708305.1	EST_HUMAN	AV708305 ADC Homo sapiens cDNA clone ADCAK806 5'
1704	6699	11775	1.99	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and olfactory-imbic associated protein AT1-46 mRNA, complete cds
1868	6953	12058	7.06	4.0E-03	AA099777.1	EST_HUMAN	Z81a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
2186	7165		1.43	4.0E-03	BE410556.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2215	7192	12314	1.14	4.0E-03	AW784740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
2498	7466	12580	1.56	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2498	7466	12581	1.56	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2619	7581	12691	2.52	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2619	7581	12682	2.52	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2624	7585	12695	1.04	4.0E-03	AL169284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3154	8170	13181	1.06	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151289-003-h08 HT0340 Homo sapiens cDNA
3154	8170	13192	1.06	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151289-003-h08 HT0340 Homo sapiens cDNA
3452	8460	13486	0.82	4.0E-03	AW188426.1	EST_HUMAN	X98804.x1 NCL CGAP_Co18 Homo sapiens cDNA clone IMAGE:2665279 3'
3452	8460	13487	0.82	4.0E-03	AW188426.1	EST_HUMAN	X98804.x1 NCL CGAP_Co18 Homo sapiens cDNA clone IMAGE:2665279 3'
3815	8548	13558	1.02	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3889	8889		1.73	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
4480	9470	14451	1.08	4.0E-03	A1792754.1	EST_HUMAN	ab18a08.x5 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
370	5419	10434	2.62	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
868	5886	10928	5.77	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1621	6618	11684	2.72	3.0E-03	AA468110.1	EST_HUMAN	nc73c05.s1 NCL CGAP_P12 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2231	7208		7.09	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triphosphate isomerase
2232	7209	12323	0.92	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2232	7209	12324	0.92	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2923	7942		0.93	3.0E-03	Y08006.1	NT	Arabidopsis thaliana poMt gene
3009	8026	13038	4.49	3.0E-03	BE379236.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609933 5'
3078	8094	13108	3.08	3.0E-03	AW802687.1	EST_HUMAN	IL2-UM0076-240300-056-D03 UM0076 Homo sapiens cDNA
3333	8343	13361	2.06	3.0E-03	U34606.1	NT	Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2
3342	8351		7.49	3.0E-03	Y12500.1	NT	C.elegans samdc gene
3870	8871	13878	7.05	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDS8SG01 5'
3870	8871	13877	7.05	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDS8SG01 5'
3925	8925	13915	1.6	3.0E-03	A1792278.1	EST_HUMAN	el04009.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4027	9023		1.04	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triphosphate isomerase
4271	9284	14254	4.26	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4338	8329		0.68	3.0E-03	BE348739.1	EST_HUMAN	h68g08.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151934 3'
4387	8378	14359	5.15	3.0E-03	A1536141.1	EST_HUMAN	xu8.P10.H3 conorm Homo sapiens cDNA 3'
4886	8671	14653	2.19	3.0E-03	A1732754.1	EST_HUMAN	ab18a08.x5 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
4705	9690	14673	6.10	3.0E-03	BE787845.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
4988	8945	14822	0.92	3.0E-03	4508414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
4988	8945	14823	0.92	3.0E-03	4508414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5014	9985	14961	0.88	3.0E-03	S82213.1	NT	CD11b=leukocyte integrin alpha chain (human, Genomic, 104 nt, segment 23 of 31)
511	5548	10550	0.69	2.0E-03	Q04852	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
511	5548	10551	0.69	2.0E-03	Q04852	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
777	7731		10.87	2.0E-03	T70874.1	EST_HUMAN	yf16h03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108341 5'
1348	6343	11394	1.92	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1348	6345	11396	1.98	2.0E-03	AA681605.1	EST_HUMAN	nu86f01.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217593
1357	6354	11404	8.74	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
							PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD161 ANTIGEN)
1458	6455	11514	4.39	2.0E-03	P48509	SWISSPROT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1485	6482	11537	1.7	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1485	6482	11538	1.7	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1558	6553		4.37	2.0E-03	P28400	SWISSPROT	COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR
1734	6729	11808	1.16	2.0E-03	AA460138.1	EST_HUMAN	z42a10.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
1949	6935	12036	1.19	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2188	7167	12287	1.03	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C10?
2504	7472		3.15	2.0E-03	AW137782.1	EST_HUMAN	UI-H-B17-adf-g-10-O-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3332	8342	13360	5.57	2.0E-03	AA450138.1	EST_HUMAN	z42a10.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3338	8347	13365	0.86	2.0E-03	BF568955.1	EST_HUMAN	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
							H. sapiens DMA, DMB, HLA-Z1, IIP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
3582	8589	13593	5.61	2.0E-03	X87344.1	NT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP38]
3997	8993	13980	2.35	2.0E-03	P03374	SWISSPROT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4099	9093		8.68	2.0E-03	U68491.1	NT	UI-H-BW0-air-g-03-O-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2730413 3'
4303	9295		1.17	2.0E-03	AW297380.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA
4307	9299	14285	0.82	2.0E-03	A1064746.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4415	9405	14390	2.22	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4415	9405	14391	2.22	2.0E-03	L42512.1	NT	yo45602.s1 Soares adult brain N2b4HB58Y Homo sapiens cDNA clone IMAGE:180890 3'
4573	9561		1.9	2.0E-03	R87773.1	EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
							regions
4861	9842	14814	0.94	2.0E-03	AF003528.1	NT	y98c08.r1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
436	5474	10490	1.26	1.0E-03	H68471.1	EST_HUMAN	as70508.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
819	5839	10876	1.31	1.0E-03	A1720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;

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Table 4
Single Exon Probes Expressed in HBL100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
819	5839	10877	1.31	1.0E-03	A172063.1	EST_HUMAN	as70608.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
1078	6085	11114	3.35	1.0E-03	A186788.1	EST_HUMAN	Q13825 AL-BINDING PROTEIN/ENOYL-COA HYDRATASE ;
1098	6105	11135	1.17	1.0E-03	A1854572.1	EST_HUMAN	wk86a06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3'
							wx23e10.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'
1148	6152	11184	4.08	1.0E-03	A1692616.1	EST_HUMAN	wd86a01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu repetitive element;
1977	6962	12669	2.88	1.0E-03	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMWMI)
2093	7074	12188	4.54	1.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
2911	7930	12949	1.8	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for KIAA1291 protein, partial cds
3118	8134	13153	2.17	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3118	8134	13154	2.17	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3228	8243	13265	0.75	1.0E-03	P08547	SWISSPROT	CARBONIC ANHYDRASE (SALIVARY CARBONIC ANHYDRASE)
3468	8474	13498	0.76	1.0E-03	U68051.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3468	8474	13499	0.76	1.0E-03	U68051.1	NT	CARBONIC ANHYDRASE (SALIVARY CARBONIC ANHYDRASE)
3581	8588		1.51	1.0E-03	AB044400.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3831	8833	13840	0.76	1.0E-03	Z49849.1	NT	Human MUC2 gene, promoter region
4312	9304	14288	5.29	1.0E-03	BE839162.1	EST_HUMAN	Human MUC2 gene, promoter region
4349	9340	14321	4.94	1.0E-03	BE246536.1	EST_HUMAN	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4528	9518	14505	0.91	1.0E-03	U28449.1	NT	S. cerevisiae chromosome X reading frame ORF YJR149w
4677	9682	14844	1.69	1.0E-03	A1073485.1	EST_HUMAN	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4677	9682	14845	1.69	1.0E-03	A1073485.1	EST_HUMAN	TCBAP1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4909
4678	9663		5.57	1.0E-03	BE154087.1	EST_HUMAN	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4905	9884	14855	8.4	1.0E-03	O46409	SWISSPROT	ov45c04.x1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:1640262 3'
							ov45c04.x1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4896	9875	14843	1.32	9.0E-04	AA815400.1	EST_HUMAN	PMO-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
4056	9050		4.35	8.0E-04	P08547	SWISSPROT	APOLIPROTEIN A-IV PRECURSOR (APO-AIV)
4819	9604	14592	2.42	8.0E-04	U28185.1	NT	ai61c12.s1 Soares_testis NHT Homo sapiens cDNA clone 1375318 3' similar to SW:AATC_CHICK P00504
2335	7309	12430	1.75	7.0E-04	U29185.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
2642	7602	12715	1.09	7.0E-04	AL163210.2	NT	Homo sapiens prion protein (PrP) gene, complete cds
3207	8222	13244	1.03	7.0E-04	4885170	NT	Homo sapiens prion protein (PrP) gene, complete cds
3953	8855	13860	1.51	8.0E-04	A182525.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
							Homo sapiens chromosome X open reading frame 8 (CXORF6) mRNA
							wf15a1.1.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3'

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4060	9054	14041	3.01	6.0E-04	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
643	5871	10875	10.72	5.0E-04	O10341	SWISSPROT	HYPOTHETICAL 28.3 KD PROTEIN (ORF92)
1472	6469		1.4	5.0E-04	AW851844.1	EST_HUMAN	QV0-CT0225-021099-030-a07 CT0225 Homo sapiens cDNA
							nk27e11.s1 NCL CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element;
3329	8339	13357	1.21	5.0E-04	AA548931.1	EST_HUMAN	Haemophilus influenzae Rd section 63 of 163 of the complete genome
665	5691	10700	1.07	4.0E-04	U32748.1	NT	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
837	5856	10896	1.34	4.0E-04	A1720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENYOYL-COA HYDRATASE.1
							as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
837	5856	10897	1.34	4.0E-04	A1720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENYOYL-COA HYDRATASE.1
1437	6434	11491	2.18	4.0E-04	AW763368.1	EST_HUMAN	RC3-CT0254-130100-023-101 CT0254 Homo sapiens cDNA
2030	7013	12122	1.19	4.0E-04	AL163276.2	NT	Homo sapiens chromosome 21 segment HS21C078
2075	7057		0.94	4.0E-04	AL048704.1	EST_HUMAN	DKFZp434D059.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D059 5'
2554	7519	12636	2.01	4.0E-04	O96615	SWISSPROT	SERPIN-2 (SILK GUM PROTEIN 2)
3091	8107	13123	3.3	4.0E-04	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3776	8778		1.12	4.0E-04	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
							nh10a10.s1 NCL CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4196	9189	14169	2.79	4.0E-04	AA576331.1	EST_HUMAN	nh10a10.s1 NCL CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4196	9189	14170	2.79	4.0E-04	AA576331.1	EST_HUMAN	nh10a10.s1 NCL CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4407	9398	14362	2.39	4.0E-04	AA086324.1	EST_HUMAN	zn61c08.s1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:562670 3'
4915	9883	14867	3.42	4.0E-04	BE560660.1	EST_HUMAN	60134595F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5'
							yy78b10.s1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:278643 3' similar to contains Alu repetitive element;
5019	9990	14965	1.02	4.0E-04	N48313.1	EST_HUMAN	DKFZp761J221.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J221 5'
155	5221	10233	2.94	3.0E-04	AL118426.1	EST_HUMAN	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
195	5259	10272	1.5	3.0E-04	P49259	SWISSPROT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
889	5887	10929	2.14	3.0E-04	U83991.1	NT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1803	6794	11884	1.69	3.0E-04	AI262100.1	EST_HUMAN	qz28403.y1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028197 5'
1817	6807		2.03	3.0E-04	AI99874.1	EST_HUMAN	h23a02.x1 NCL CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2119082 3'
3236	8250	13271	4.06	3.0E-04	P25147	SWISSPROT	INTERNALIN B PRECURSOR
3857	8859	13665	3.31	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
3942	8940		1.31	3.0E-04	AI271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
3978	8974		1.09	3.0E-04	BE140609.1	EST_HUMAN	RCO-HT0014-310599-028 HT0014 Homo sapiens cDNA
4671	9656		5.1	3.0E-04	BE153778.1	EST_HUMAN	PMO-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
175	6239	10250	1.52	2.0E-04	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
475	5511	10524	5.11	2.0E-04	AU148707.1	EST_HUMAN	AU148707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
896	5914	10953	6.36	2.0E-04	M86524.1	NT	Human dystrophin gene
896	5914	10954	6.36	2.0E-04	M86524.1	NT	Human dystrophin gene
1160	6164		3.63	2.0E-04	AI286021.1	EST_HUMAN	qh98e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
1167	6170		2.07	2.0E-04	AL163203.2	NT	MER3.b2 MER3 repetitive element;
1788	6787		0.97	2.0E-04	AF224288.1	NT	Homo sapiens chromosome 21 segment HS21C003
2120	7100		1.21	2.0E-04	AA478980.1	EST_HUMAN	Mus musculus 5' flanking region of Plb3 gene
							z199b05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element;
2500	7468	12583	3.15	2.0E-04	U66081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV14S1, TCRBV16S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY8, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2;>
2918	7937	12954	1.18	2.0E-04	AI124529.1	EST_HUMAN	am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3260	8273	13288	1.1	2.0E-04	BE082317.1	EST_HUMAN	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3351	8360	13376	2.67	2.0E-04	U34374.1	NT	QV2-BT0636-070500-104-b07 BT0636 Homo sapiens cDNA
3381	8389	13412	0.91	2.0E-04	AW978441.1	EST_HUMAN	Human tyrosine kinase TXK (tk) gene, exons 9 and 10
3816	8818	13825	1.04	2.0E-04	U01029.1	NT	EST390550 IMAGE resequences, MAGP Homo sapiens cDNA
4020	8016		5.78	2.0E-04	U01029.1	NT	Phaseolus vulgaris nitrate reductase (PVNR2) gene, complete cds
4534	9524	14511	1.51	2.0E-04	H96265.1	EST_HUMAN	y007e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4534	9524	14512	1.51	2.0E-04	H96265.1	EST_HUMAN	y007e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4651	8636		1.39	2.0E-04	U09228.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
4891	9870	14838	1.87	2.0E-04	AB037997.1	NT	Danio rerio hagerorn gene, exons 1 to 8, partial cds
758	5778	10808	1.09	1.0E-04	H99548.1	EST_HUMAN	y226c09.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:262884 3' similar to contains L1.1 L1 repetitive element;
1058	6067	11097	1.86	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1097	6104	11133	3.05	1.0E-04	AW013947.1	EST_HUMAN	UI-H-B10-aab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1097	6104	11134	3.05	1.0E-04	AW013947.1	EST_HUMAN	UI-H-B10-aab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1312	6309		3.3	1.0E-04	U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1588	6585	11646	3.97	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1588	6585	11647	3.97	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1824	6814	11908	1.7	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY36
3211	8226	13248	0.96	1.0E-04	Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
3651	8657	13663	0.72	1.0E-04	A1440282.1	EST_HUMAN	g01f11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
3948	8948	13926	1.86	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
3967	8966	13955	1.09	1.0E-04	AV847727.1	EST_HUMAN	AV847727 GLC Homo sapiens cDNA clone GLCBBD04 3'
4925	8902	14878	1.64	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237) mRNA
4925	8902	14879	1.64	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237) mRNA
689	5713	10727	1.84	9.0E-05	AA718933.1	EST_HUMAN	ah45c11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1282468 3'
811	5632	10865	1.19	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
853	5872		12.78	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
4353	9344	14323	0.67	8.0E-05	AW044605.1	EST_HUMAN	wy78a04.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
345	5397	10404	11.8	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220989-011-E04 CT0208 Homo sapiens cDNA
345	5397	10405	11.8	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220989-011-E04 CT0208 Homo sapiens cDNA
502	5596	10595	1.24	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
582	5596	10596	1.24	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
1038	6048	11078	1.43	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2846	7606	12718	2.46	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C073
3085	8101	13116	4.38	7.0E-05	AB009080.1	NT	Dicystotellum discoidium gene for TRPA, complete cds
3617	8824		1.24	7.0E-05	AI432413.1	EST_HUMAN	ig73c09.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2114416 3'
3943	8941		0.72	7.0E-05	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4247	9241	14225	1.61	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4769	9753	14741	0.66	7.0E-05	9845300	NT	Rat cytomegalovirus Maastricht, complete genome
1976	6861	12067	1.9	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
1976	6961	12068	1.6	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2513	7481	12597	1.15	6.0E-05	A1655241.1	EST_HUMAN	w54h08.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb:J03250 DNA TOPOISOMERASE I (HUMAN);
2742	5686	10704	2.86	6.0E-05	AF0563630.1	NT	Homo sapiens monocytic/neutrophil elastase inhibitor gene, complete cds
1379	6376	11424	65.3	5.0E-05	AW392086.1	EST_HUMAN	QV4-ST0234-241189-040-h11 ST0234 Homo sapiens cDNA
1826	6818		2.39	5.0E-05	8923891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55895), mRNA
2780	7811	12828	0.67	5.0E-05	AJ251058.1	NT	Homo sapiens MEPIA gene, promoter region and exon 1
3872	8873	13878	4.04	5.0E-05	AJ251884.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
2735	5289		3.87	4.0E-05	U12821.1	NT	Human retin (REN) gene, 5' flanking region
4355	9348	14325	0.92	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4355	9348	14326	0.92	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4725	9710		0.99	4.0E-05	AF164488.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
672	5697	10706	0.69	3.0E-05	AJ248081.1	EST_HUMAN	qh64c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element ;
1042	6052	11082	1.01	3.0E-05	AW273851.1	EST_HUMAN	x124g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1114	6120	11148	1.64	3.0E-05	BF037898.1	EST_HUMAN	601481463F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3865142 5'
1114	6120	11149	1.64	3.0E-05	BF037898.1	EST_HUMAN	601481463F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3865142 5'
2848	7608	12720	0.92	3.0E-05	Q62234	SWISSPROT	SKELEMIN
4257	9251	14237	9.42	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4257	9251	14238	9.42	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4342	9333	14316	0.94	3.0E-05	AA368879.1	EST_HUMAN	EST79996 Placenta Homo sapiens cDNA similar to similar to p53-associated protein
4342	9333	14317	0.94	3.0E-05	AA368879.1	EST_HUMAN	EST79996 Placenta Homo sapiens cDNA similar to similar to p53-associated protein
4486	9476	14456	0.76	3.0E-05	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4695	9680	14663	0.93	3.0E-05	AU125721.1	EST_HUMAN	AU125721 NT2RM4 Homo sapiens cDNA clone NT2RM4002075 5'
							qh98e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
2282	7239	12358	1.33	2.0E-05	AJ286021.1	EST_HUMAN	MER3.b2 MER3 repetitive element ;
2506	7474	12589	1.85	2.0E-05	M13792.1	NT	Human adenosine deaminase (ADA) gene, complete cds
							zq46a12.1r1 Stralagene hNT_neuron (#937233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element ;
2641	7601		5.26	2.0E-05	AA160562.1	EST_HUMAN	RC3-BT0319-120200-014-H08 BT0319 Homo sapiens cDNA
3064	8081	13095	1.66	2.0E-05	BE08036.1	EST_HUMAN	Homo sapiens p47-phox (NCF1) gene, complete cds
3272	8284	13307	0.85	2.0E-05	AF184614.1	NT	H. sapiens DNA for endogenous retroviral like element
3287	8298	13325	1.06	2.0E-05	X89211.1	NT	S. cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
3414	8423		0.69	2.0E-05	X95465.1	NT	Homo sapiens chromosome 21 segment HS21C062
2623	7777	12894	1.66	1.0E-05	AL163282.2	NT	Homo sapiens melanogaster strain Lamto 120 Suppressor of Hairless (Su(H)) gene, partial cds
3565	8572	13578	2.01	1.0E-05	AF088273.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3723	8727		1.18	1.0E-05	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3860	8882	13887	10.08	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4049	9045	14033	1.04	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4155	9150	14132	1.76	1.0E-05	AA431119.1	EST_HUMAN	zw69g04.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:781494 5'
4703	8688	14671	1.9	1.0E-05	AW419134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
2601	7563	12881	2.89	9.0E-06	AI583811.1	EST_HUMAN	tt73a06.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246388 3'
3022	8039	13048	4.56	9.0E-06	AI218983.1	EST_HUMAN	qg11b08.x1 Soares placenta 8to8weeks_2NbHP8(s9W Homo sapiens cDNA clone IMAGE:1759191 3'
3529	8535		2.84	9.0E-06	M81765.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
2458	7771	12543	1.52	8.0E-06	AW382539.1	EST_HUMAN	RC3-CT0283-201199-011-h11 CT0283 Homo sapiens cDNA
964	5979		1.3	7.0E-06	AA669729.1	EST_HUMAN	ab90f10.s1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains
1412	6410	11469	2.42	7.0E-06	7662177	NT	MER20.11 MER20 repetitive element ;
2802	7822		6.98	7.0E-06	AI368252.1	EST_HUMAN	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2847	7867	12883	1.16	6.0E-06	BE069189.1	EST_HUMAN	qw16g09.x1 NCI_CGAP_U3 Homo sapiens cDNA clone IMAGE:1891298 3' similar to contains Alu repetitive element;
2871	7890	12912	1.03	6.0E-06	Q01456	SWISSPROT	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
3608	8616	13825	0.93	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
4609	7890	12912	1.96	6.0E-06	Q01456	SWISSPROT	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
4616	8601	14587	2.14	6.0E-06	AI040099.1	EST_HUMAN	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
639	5687	10670	5.76	4.0E-06	R16267.1	EST_HUMAN	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
836	5855	10895	6.98	4.0E-06	AW103354.1	EST_HUMAN	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
1314	6311	11369	3.35	4.0E-06	AI34928.1	EST_HUMAN	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
1314	6311	11360	3.35	4.0E-06	AI34928.1	EST_HUMAN	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
1445	6442	11500	1.85	4.0E-06	BF365612.1	EST_HUMAN	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
2203	7181	12304	1.59	4.0E-06	AW015401.1	EST_HUMAN	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
2990	8008	13021	0.74	4.0E-06	AF188349.1	NT	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
3789	8802	13807	1.07	4.0E-06	AW848295.1	EST_HUMAN	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
4663	9848	14635	1.95	4.0E-06	AI886939.1	EST_HUMAN	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5047	10018	14987	1.04	4.0E-06	AW817268.1	EST_HUMAN	QV0-ST0247-090200-105-c05 ST0247 Homo sapiens cDNA
2099	7080	12194	1.29	3.0E-06	AA700582.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.t1 L1 repetitive element;
2099	7080	12195	1.29	3.0E-06	AA700582.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.t1 L1 repetitive element;
2205	7182		1.19	3.0E-06	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
2851	7871	12886	1.09	3.0E-06	AA868218.1	EST_HUMAN	ak48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13 LTR1 repetitive element;
3191	8207		2.25	3.0E-06	A1857779.1	EST_HUMAN	w22a05.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734 LINE-1 LIKE PROTEIN; contains L1.12 L1 repetitive element;
3695	8699	13701	1.73	3.0E-06	BE047094.1	EST_HUMAN	hq84d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
3695	8699	13702	1.73	3.0E-06	BE047094.1	EST_HUMAN	hq84d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4430	9420	14406	2.51	3.0E-06	X54816.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
4768	9750	14738	0.95	3.0E-06	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
4768	9750	14739	0.95	3.0E-06	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
202	5268		2.36	2.0E-06	P54366	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
1535	6533		4.34	2.0E-06	P21414	SWISSPROT	POLYPROTEINCONTAINS: PROTEASE: REVERSE TRANSCRIPTASE: ENDONUCLEASE]
2315	7290	12411	3.21	2.0E-06	A1672138.1	EST_HUMAN	w804a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30.b1 MER30 repetitive element;
2397	7368	12489	1.48	2.0E-06	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2494	7462	12577	4.19	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3441	8449	13475	1.07	2.0E-06	AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLOCDB05 3'
3676	8681	13684	1.7	2.0E-06	AA173518.1	EST_HUMAN	zp02e05.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595232 5'
3689	8693	13695	1.8	2.0E-06	AB030896.1	NT	Mus musculus gene for odorant receptor A16, complete cds
34	5114	10100	1.11	1.0E-06	O76082	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE CO-TRANSPORTER)
649	5877	10684	1.24	1.0E-06	AF084364.1	NT	Mus musculus D6Mm5E protein (D6Mm5e) mRNA, complete cds
1425	6422	11481	1.53	1.0E-06	P09125	SWISSPROT	MEROZOITE SURFACE PROTEIN CMZ-8
1491	6489	11544	0.92	1.0E-06	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
1848	6934	12034	3.32	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
1948	6934	12035	3.32	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4244	9238	14221	13.65	1.0E-06	U07551.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4833	9910	14887	1.24	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4833	9910	14888	1.24	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
359	5409	10421	1.02	9.0E-07	AF003629.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
359	5409	10422	1.02	9.0E-07	AF003629.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
4625	9610	14598	5.07	8.0E-07	AI288596.1	EST_HUMAN	ql82g07.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
4625	9610	14599	5.07	8.0E-07	AI288596.1	EST_HUMAN	ql82g07.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
1888	6857	11945	2.73	6.0E-07	AW855558.1	EST_HUMAN	CM3-CT0277-221099-024-e11 CT0277 Homo sapiens cDNA
							Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (BF), and complement component C2 (C2) genes, >
2421	7392	12513	2.45	6.0E-07	AF019413.1	NT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION
3885	8867		1.99	6.0E-07	P41479	SWISSPROT	wh64f10.x1 NCI_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
324	5378		0.9	5.0E-07	AB31893.1	EST_HUMAN	EST193615 Supt cells Homo sapiens cDNA 5' end
1040	6050		1.83	5.0E-07	AA380630.1	EST_HUMAN	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
4511	8501	14480	1.28	5.0E-07	AF149774.1	NT	ws84h08.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504697 3'
3893	8893	13892	1.86	4.0E-07	AW006802.1	EST_HUMAN	Human microfibril-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
438	5476	10492	5.45	3.0E-07	U19719.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
578	5610	10609	2.79	3.0E-07	AJ271735.1	NT	Human polymorphic microsatellite DNA
1366	6353	11403	1.32	3.0E-07	M99149.1	NT	Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 allele
1588	6583		1.79	3.0E-07	M64857.1	NT	Human polymorphic microsatellite DNA
2224	7201	12320	0.94	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
2399	7370	12491	26.28	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-111 BN0115 Homo sapiens cDNA
2399	7370	12492	26.28	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-111 BN0115 Homo sapiens cDNA
2884	7982	12896	0.85	3.0E-07	T84704.1	EST_HUMAN	y450f12.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:111695 5'
3086	8102	13117	1.84	3.0E-07	P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4587	9575	14566	8.15	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCCD01 3'
							yc14h09.s1 StrataGene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
4895	9874	14841	1.6	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 StrataGene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
4895	9874	14842	1.6	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 StrataGene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
29	5109	10094	2.94	2.0E-07	AF262988.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
153	5218	10231	23.84	2.0E-07	L77669.1	NT	Homo sapiens DGeorge syndrome critical region, telomeric end
153	5219	10232	23.84	2.0E-07	L77669.1	NT	Homo sapiens DGeorge syndrome critical region, telomeric end
181	5244	10265	129.68	2.0E-07	U38849.1	NT	Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
739	5762	10785	1.46	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
739	5762	10786	1.46	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
929	5946	10980	1.99	2.0E-07	AA223260.1	EST_HUMAN	z08b07.s1 Stralagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869 3' similar to gb:L31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element;
930	5947	10981	11.68	2.0E-07	T63042.1	EST_HUMAN	yc15g04.s1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element;
1145	6149	11181	0.93	2.0E-07	Q26768	SWISSPROT	I/6 AUTOANTIGEN
1565	6562	11625	2.13	2.0E-07	Q09701	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME 1
3604	8611	13619	20.05	2.0E-07	AF126348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
1085	6092		1.43	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2754	6488	11543	2.14	1.0E-07	P09256	SWISSPROT	GLYCOPROTEIN GPV
3659	6092		3.91	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4169	9164	14150	2.86	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
4169	9164	14151	2.86	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
4973	8949	14927	1.22	1.0E-07	AA019181.1	EST_HUMAN	ze56g02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363026 5'
604	7725		2.23	8.0E-08	AI911352.1	EST_HUMAN	wd18b05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3943976 5'
1033	6043		0.8	8.0E-08	BE795469.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
3468	8476		1.7	8.0E-08	BE795469.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
78	5158	10167	3.2	7.0E-08	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
1344	6341	11392	42.98	7.0E-08	X04809.1	NT	Rat mRNA for ribosomal protein L31
3495	8503	13517	0.7	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
3495	8503	13518	0.7	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
807	5828	10859	2.78	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C043
807	5828	10859	2.78	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C043
2302	7277	12397	3.8	6.0E-08	BE144398.1	EST_HUMAN	MR0-HT0166-191166-004-g09 HT0166 Homo sapiens cDNA
2988	8006	13019	2.09	8.0E-08	7662473	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4126	9121	14103	0.92	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
83	5160	10171	2.15	5.0E-08	AL163003.2	NT	Homo sapiens chromosome 21 segment HS21C103
2174	7163	12273	1.68	5.0E-08	AA493851.1	EST_HUMAN	nt03569.s1 NC1_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943183 similar to contains Alu repetitive element;
1722	6717	11763	1.2	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1722	6717	11794	1.2	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
2816	7835		1.1	4.0E-08	AL079581.1	EST_HUMAN	DKFZp434J0426_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434J0426 5'

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
206	5270		8.87	2.0E-08	AW302996.1	EST_HUMAN	x8706.x1 NCL_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767139 3'
227	5280		7.99	2.0E-08	AA425598.1	EST_HUMAN	z44807.r1 Soares_tetol_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element; contains element MER15 repetitive element;
493	5529	10537	2.63	2.0E-08	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
652	5680	10586	9.13	2.0E-08	AW886438.1	EST_HUMAN	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
652	5680	10587	9.13	2.0E-08	AW886438.1	EST_HUMAN	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
975	5991		28.56	2.0E-08	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
1323	6321	11369	1.74	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1702	6697		1.75	2.0E-08	BE734871.1	EST_HUMAN	601570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845199 5'
1818	6808		3.33	2.0E-08	AW270271.1	EST_HUMAN	XP4311.x1 NCL_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2352	7326	12443	1.22	2.0E-08	AA731948.1	EST_HUMAN	nm64h01.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1251409 3' similar to contains L1.t3 L1 repetitive element;
2472	7441		1.31	2.0E-08	K00216.1	NT	Sheep His-IRNA-GUG
3135	8151	13173	6.15	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3135	8151	13174	6.15	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3769	8772		1.61	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0197-161099-012-b03 ST0197 Homo sapiens cDNA
4281	9274		1.32	2.0E-08	AA459040.1	EST_HUMAN	aa26c07.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.t2 L1 repetitive element;
4800	9784		3.44	2.0E-08	AW572881.1	EST_HUMAN	he17h08.x2 NCL_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains Alu repetitive element;
1738	6733	11810	1.28	1.0E-08	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
1998	6981		1.58	1.0E-08	BE141959.1	EST_HUMAN	PM2-HT0130-150999-001-f12 HT0130 Homo sapiens cDNA
3119	8135	13155	1.06	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
3119	8135	13156	1.06	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
4120	9114	14100	3.28	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
4120	9114	14101	3.28	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3526	8532		1.62	7.0E-08	D86842.1	NT	Homo sapiens DNA for 3-ketacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
4310	9302	14287	1.19	6.0E-09	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4821	9805	14787	4.99	6.0E-09	BE169421.1	EST_HUMAN	PM1-HT0527-160200-001-h05 HT0527 Homo sapiens cDNA
1390	6387	11439	2.89	5.0E-09	BE149264.1	EST_HUMAN	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA

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Table 4
Single-Event Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1816	6808	11899	1.29	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
517	5552		1.41	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
950	5568		2.28	4.0E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1441	6438	11495	2.05	4.0E-09	9558718	NT	Homo sapiens hypothetical protein (AF038169). mRNA
2362	7336	12463	17.61	4.0E-09	AA350878.1	EST_HUMAN	EST59385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 80 kDa
							Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2290	7265	12383	3.39	3.0E-09	BE222239.1	EST_HUMAN	MER18 repetitive element
							Hu09609.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2482	7450	12563	1.04	3.0E-09	BE222238.1	EST_HUMAN	PROTEIN MOV-10
2578	7541	12655	0.92	3.0E-09	P23248	SWISSPROT	MER18 repetitive element
							Hu09609.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
3254	8267	13289	1.29	3.0E-09	BE222239.1	EST_HUMAN	MER18 repetitive element
3292	8303	14281	6.3	3.0E-09	AA442272.1	EST_HUMAN	zy54a04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
4302	9294	14281	4.42	3.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
4381	9372	14351	1.63	3.0E-09	Q973R5	SWISSPROT	258.1 kDa PROTEIN C21ORF5 (KIAA0933)
1239	6237	11280	13.77	2.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1618	6616		14.81	2.0E-09	AL118573.1	EST_HUMAN	DKFZp761B1710_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5'
2265	7242	12359	8.68	2.0E-09	Q973R5	SWISSPROT	258.1 kDa PROTEIN C21ORF5 (KIAA0933)
3834	8836	13842	3.1	2.0E-09	O60241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
1092	6099	11128	1.68	1.0E-09		SWISSPROT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1092	6099	11129	1.68	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
					5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
2428	7399		1.35	1.0E-09	A1356086.1	EST_HUMAN	qy64e11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2016812 3' similar to contains MER12.12
							MER12 repetitive element
2819	7839	12856	1.69	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (simn) genes, complete cds
2855	7875	12890	17.33	1.0E-09	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
2855	7875	12891	17.33	1.0E-09	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
2866	7884	12998	0.69	1.0E-09	BE535440.1	EST_HUMAN	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
							601058602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
4654	8639		6.25	1.0E-09	AA719297.1	EST_HUMAN	zh35b03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains
1260	6289	11333	1.94	9.0E-10	AW867740.1	EST_HUMAN	Alu repetitive element:contains element MER22 repetitive element
							MR0-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
2760	7781	12806	7.26	9.0E-10	A1870071.1	EST_HUMAN	we78h03.x1 Soares_Dieckgraefe_color_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to
							SW:RL28_HUMAN P47914.60S RIBOSOMAL PROTEIN L29 ; contains element P175 repetitive element

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
146	5212	10228	11.08	8.0E-10	U63630.2	NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
4078	9072	14059	1.87	8.0E-10	AA376832.1	EST_HUMAN	EST195584 Small Intestine 1 Homo sapiens cDNA 5' end
692	5716	10732	39.41	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
692	5716	10733	39.41	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
1563	6580	11843	1.69	7.0E-10	Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
2488	7456		9.17	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3014	8031	13041	2.59	7.0E-10	X00856.1	NT	H. sapiens DHFR gene, exon 3
							Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
902	5920	10958	2.89	6.0E-10	AJ400877.1	NT	gene
2608	7588	12883	1.11	6.0E-10	AI424405.1	EST_HUMAN	h02d07.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2085021 3'
4598	9586		2.92	6.0E-10	AW853718.1	EST_HUMAN	RC3-CT0254-031099-012-g12 CT0254 Homo sapiens cDNA
751	5773		4.91	5.0E-10	AL046804.1	EST_HUMAN	DKFZp434N219_11 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N219 5'
3395	8403	13429	1.16	5.0E-10	Q01033	SWISSPROT	HYPOTHETICAL GENE 48 PROTEIN
4833	9817	14785	1.25	5.0E-10	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
							qg09f09.x1 Soares, placenta, 8to9weeks, 2NbhP8to9W Homo sapiens cDNA clone IMAGE:1758049 3'
111	5183		1.48	4.0E-10	A1221083.1	EST_HUMAN	similar to contains LTR8.b2 LTR8 repetitive element
576	5608	10607	1.35	4.0E-10	AA515260.1	EST_HUMAN	h64a01.s1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:924648 3'
							hg56g03.x1 NCI_CGAP_GC08 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu repetitive element
1950	6936	12037	1.15	4.0E-10	AW594709.1	EST_HUMAN	repetitive element
2499	7467	12582	3.14	4.0E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
							yy62f06.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.t1 L1 repetitive element
904	5921	10958	1.72	3.0E-10	N36113.1	EST_HUMAN	Homo sapiens extracellular glycoprotein lactacin precursor, gene, complete cds
1333	6331		4.3	3.0E-10	AY005150.1	NT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
36	5116	10102	1.49	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
36	5116	10103	1.49	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
							Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (srin) genes, complete cds
1857	6846		2.98	2.0E-10	U80017.1	NT	protein (nail) and survival motor neuron protein (srin) genes, complete cds
2917	7936		1.37	2.0E-10	BF675047.1	EST_HUMAN	602136640F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
1479	6476		1.01	1.0E-10	AW867767.1	EST_HUMAN	MRO-SN0038-290300-001-001 SN0038 Homo sapiens cDNA
1570	6567	11629	2.18	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCCXA11 3'
2505	7473		2.43	1.0E-10	AW852001.1	EST_HUMAN	QV0-C10225-161169-058-e08 CT0225 Homo sapiens cDNA
3420	8428	13454	0.69	1.0E-10	AW832912.1	EST_HUMAN	QV2-TT0003-161169-013-g10 TT0003 Homo sapiens cDNA
3462	8470		0.97	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_11 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
3754	8470		1.16	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_11 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3908	8908		6.83	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4007	9003	13990	4.83	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4007	9003		4.83	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4013	9009	13991	4.83	1.0E-10	AB031069.1	NT	Homo sapiens PGCX1 mRNA for protein containing CXXC domain 1, complete cds
4046	9042	13999	2.35	1.0E-10	M30626.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
259	5318	10328	1.16	9.0E-11	BE145600.1	EST_HUMAN	IL2-1-T0203-281099-018-c08 HT0203 Homo sapiens cDNA clone DKFZp547D225 5'
2046	7028	12139	4.32	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
2046	7028	12140	4.32	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
3299	8310	13337	2.54	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
3299	8310	13338	2.54	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
4371	9363	14343	0.69	9.0E-11	AA775985.1	EST_HUMAN	as78101.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:370297 3'
3042	8059		8.11	8.0E-11	H19971.1	EST_HUMAN	yn53111.s1 Soares adult brain N2b5H855Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element
3930	8930	13921	4.2	8.0E-11	N23712.1	EST_HUMAN	yw46908.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
1422	6419	11479	1.51	7.0E-11	AA330842.1	EST_HUMAN	EST34392 Embryo, 6 week Homo sapiens cDNA 5' end
409	5448	10467	5.12	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
409	5448	10468	5.12	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
12	5092	10076	0.93	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3284	6092	10076	0.92	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4107	9101	14088	1.53	5.0E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
1377	6374		5.75	4.0E-11	AA436042.1	EST_HUMAN	zu01b12.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:730559 5'
2718	7875	12788	4.93	4.0E-11	BE885900.1	EST_HUMAN	601507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3809285 5'
2900	7918	12940	1.26	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4485	9475	14455	0.75	4.0E-11	D44666.1	EST_HUMAN	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069
1460	6457	11516	18.61	3.0E-11	6879077	NT	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
2828	7849		0.91	3.0E-11	AI815933.1	EST_HUMAN	wj35d08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2404811 3'
4154	9149		1.05	3.0E-11	AA309248.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
945	5962	10995	1.02	2.0E-11	AI150502.1	EST_HUMAN	q36c04.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1166	6169	11204	3.84	2.0E-11	R24807.1	EST_HUMAN	y943e12.1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1168	6169	11205	3.84	2.0E-11	R24807.1	EST_HUMAN	y943e12.1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1576	6573	11634	3.97	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3beta (COR3beta) genes, complete cds
1576	6573	11635	3.97	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3beta (COR3beta) genes, complete cds
2691	7649	12763	0.93	2.0E-11	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
3123	8139	13161	5.68	2.0E-11	P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3251	8264	13285	0.74	2.0E-11	A1478617.1	EST_HUMAN	tm64c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161936 3'
3417	8425		0.94	2.0E-11	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
4321	9313		1.04	2.0E-11	BE065537.1	EST_HUMAN	RC3-BT0316-170200-014-e05 BT0316 Homo sapiens cDNA
4474	9464		0.75	2.0E-11	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
4778	9763		1.84	2.0E-11	BE062558.1	EST_HUMAN	QV2-BT0258-261099-014-a01 BT0258 Homo sapiens cDNA
668	5693	10702	0.79	1.0E-11	AJ131016.1	NT	Homo sapiens SOL gene locus
775	5797	10825	1.24	1.0E-11	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1198	6199	11235	2.94	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1468	6466		1.4	1.0E-11	AF119914.1	NT	Homo sapiens PRO3078 mRNA, complete cds
1986	6971	12075	1.14	1.0E-11	P16258	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2067	7049	12157	2.2	1.0E-11	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxigenase gene, complete cds
3419	8427	13453	0.93	1.0E-11	BE004315.1	EST_HUMAN	GM0-BND105-170300-292-d12 BN0105 Homo sapiens cDNA
4526	9516	14502	1.42	7.0E-12	Q05904	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
3471	8479		0.75	6.0E-12	AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAW08 5'
4222	9216	14185	9.87	6.0E-12	AA732516.1	EST_HUMAN	m28811.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element
5074	10043	15009	1.48	6.0E-12	M22486.1	NT	Human chromosome 21 distal long arm DNA
1026	6036	11068	2.25	5.0E-12	T06573.1	EST_HUMAN	EST04462 Fetal brain, Striatum (cat#936206) Homo sapiens cDNA clone HFBDV33
3306	8317	13343	1.16	5.0E-12	BE047779.1	EST_HUMAN	tz42b05.y1 NCI_CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2281217 5'
3644	8650	13656	7.07	5.0E-12	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
242	5303	10313	4.12	4.0E-12	AA700326.1	EST_HUMAN	z174g11.s1 Scores fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
243	5303	10313	6.02	4.0E-12	AA700326.1	EST_HUMAN	z174g11.s1 Scores fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
4487	9477	14457	0.7	4.0E-12	A1689984.1	EST_HUMAN	b261n05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE.1

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Probe SEQ ID NO:	Exon1 SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
612	5638	10641	3.43	3.0E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517
612	5639	10642	3.43	3.0E-12	AW341683.1	EST_HUMAN	O14517 SMRP.;
1613	6609	11673	1.82	2.0E-12	AW802131.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517
3388	8394	13418	0.75	2.0E-12	6754495	NT	O14517 SMRP.;
3998	8994	13981	0.85	2.0E-12	J01884.1	NT	IL5-UM0071-120400-065-e05 UM0071 Homo sapiens cDNA
3998	8994	13982	0.85	2.0E-12	J01884.1	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA
4297	9289	13789	2.34	2.0E-12	BE063509.1	EST_HUMAN	Rat U3A small nuclear RNA
4742	9727	14712	1.72	2.0E-12	O70308	SWISSPROT	Rat U3A small nuclear RNA
4742	9727	14713	1.72	2.0E-12	O70308	SWISSPROT	CNO-BT0281-031169-087-a03 BT0281 Homo sapiens cDNA
123	5192	10205	1.65	1.0E-12	AW627674.1	EST_HUMAN	TBX15 PROTEIN (T-BOX PROTEIN 15)
1941	6927		1.12	1.0E-12	AI871726.1	EST_HUMAN	TBX15 PROTEIN (T-BOX PROTEIN 15)
2897	8015	13027	1.34	1.0E-12	AF000991.1	NT	hhs0a09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.11
2897	8015	13028	1.34	1.0E-12	AF000991.1	NT	hhs0a09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains L1.b3 L1
3783	8786	13789	29.33	1.0E-12	AU132248.1	EST_HUMAN	repetitive element;
3783	8786	13790	29.33	1.0E-12	AU132248.1	EST_HUMAN	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3543	8550		1.53	9.0E-13	AJ271735.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3843	8845	13854	0.85	9.0E-13	AB029900.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
707	5731	10747	4.84	8.0E-13	U29185.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
707	5731	10748	4.84	8.0E-13	U29185.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
1802	6783	11883	2.36	8.0E-13	U80017.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
2044	7026	12137	3.41	6.0E-13	AL163207.2	EST_HUMAN	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3248	8261		0.67	5.0E-13	R78338.1	EST_HUMAN	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3313	8324		1.36	5.0E-13	AA435773.1	EST_HUMAN	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
1830	6820		9.36	4.0E-13	AW378614.1	EST_HUMAN	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
2391	7362		1.32	4.0E-13	AF003529.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
4604	9592		1.02	4.0E-13	AA454054.1	EST_HUMAN	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
179	5242		4.21	3.0E-13	AF003528.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
854	5873		6.84	3.0E-13	AA430310.1	EST_HUMAN	znc6g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781408 5'
2309	7284	12404	1.24	3.0E-13	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2408	7378		2.01	3.0E-13	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2593	7556	12670	3.02	3.0E-13	BF372962.1	EST_HUMAN	CM3-FT0100-140700-242-08 FT0100 Homo sapiens cDNA
3113	8129		2.06	3.0E-13	AA745844.1	EST_HUMAN	ob18402.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324035 3'
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
149	6215	10229	2.57	2.0E-13	U52111.2	NT	CDM protein (CDM), adrenoleukodystrophy protein >
237	5289	10310	0.88	2.0E-13	U23839.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1251	6249	11290	6.43	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3208	8223	13245	1.32	2.0E-13	BF431999.1	EST_HUMAN	nab76105.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
3428	8436	13462	1.88	2.0E-13	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
3992	8989		2.02	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
289	5346	10358	1.09	1.0E-13	S74129.1	NT	FGF-1-fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
877	6895	10936	4.81	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1316	6313	11362	1.45	1.0E-13	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
1972	6957	12062	1.73	1.0E-13	AA720574.1	EST_HUMAN	hw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13
4461	9451	14432	1.6	1.0E-13	BF340387.1	EST_HUMAN	THR repetitive element;
331	5383	10391	2.84	9.0E-14	AA781159.1	EST_HUMAN	602038009F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4185868 5'
332	5384	10392	2.83	9.0E-14	AA781159.1	EST_HUMAN	602038009F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4185868 5'
2427	7398		3.07	9.0E-14	AW861577.1	EST_HUMAN	RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA
2680	7638	12753	3.39	9.0E-14	AB038162.1	NT	RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA
3037	8054	13062	5.01	9.0E-14	AW513296.1	EST_HUMAN	Homo sapiens TFF gene cluster for trefoil factor, complete cds
3708	8712	13715	7.31	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4612	9598	14584	1.69	9.0E-14	AJ002153.1	EST_HUMAN	Segulus oedipus gene for seminal vesicle secreted protein semenogelin I
3418	8426		1.04	8.0E-14	BE468263.1	EST_HUMAN	z71c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
3849	8851		3.5	8.0E-14	R76269.1	EST_HUMAN	y72e03.r1 Soares_placenta Nb2HP Homo sapiens cDNA clone IMAGE:144786 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1590	7751		2.88	7.0E-14	AW151673.1	EST_HUMAN	x67910.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
368	5415	10428	13.89	6.0E-14	AF020503.1	NT	MER10 repetitive element ; Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
614	5841	10644	4.27	5.0E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
4886	9885	14836	1.45	5.0E-14	AW073791.1	EST_HUMAN	ASOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
1109	7739		1.59	4.0E-14	P04928	SWISSPROT	x603b05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.12 L1
1839	6829	11918	5.27	4.0E-14	AJ007873.1	EST_HUMAN	repetitive element ;
3666	8671		0.88	4.0E-14	AA046502.1	EST_HUMAN	S-ANTIGEN PROTEIN PRECURSOR
4168	9163	14149	0.8	4.0E-14	N46328.1	EST_HUMAN	Homo sapiens LGMD2B gene
935	5952	10984	1.12	3.0E-14	X95466.1	NT	2k67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
389	5427	10442	2.33	2.0E-14	AJ271736.1	NT	W73c12.s1 Soares_multiple_sclerosis_2NbHMP Homo sapiens cDNA clone IMAGE:279190 3' similar to contains L1.13 L1 repetitive element ;
389	5427	10443	2.33	2.0E-14	AL163303.2	NT	R.norvegicus mRNA for CPC2 protein
681	7727	10716	7.63	2.0E-14	AW372888.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 2/2
2324	7298		1.24	2.0E-14	7657529	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2395	7366		1.08	2.0E-14	AL163209.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2455	7425	12539	1.41	2.0E-14	AL163246.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
1050	6059	11088	1.59	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C103
1382	6379	11427	4.61	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C103
1382	6379	11428	4.61	1.0E-14	AL163268.2	NT	RC5-BT0377-091289-031-D12 BT0377 Homo sapiens cDNA
1955	6941	12043	21.53	1.0E-14	L44140.1	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
2121	7101	12213	4.33	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C009
2343	7317	12437	18	1.0E-14	AF001689.1	NT	Homo sapiens chromosome 21 segment HS21C049
2874	7893	12916	1.2	1.0E-14	P05227	SWISSPROT	Homo sapiens chromosome 21 segment HS21C069
3094	8110	13127	5.58	1.0E-14	BF335227.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C069
3094	8110	13128	5.58	1.0E-14	BF335227.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C069
3094	8110	13128	5.58	1.0E-14	BF335227.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C069
3792	8795	13800	1.7	1.0E-14	AA682994.1	EST_HUMAN	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase
4348	9339	14320	1.98	1.0E-14	AW275852.1	EST_HUMAN	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase
1541	6539	11598	1.39	8.0E-15	7427522	NT	(GGPD) gene, complete cds's
							Homo sapiens chromosome 21 segment HS21C103
							Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
							Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
							HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
							RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
							RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
							ae58c12.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
							xq39h10.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753069 3'
							Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
						NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 8, and synaptophysin genes, complete cds; and L-type calcium channel α -
2108	7088		1.04	9.0E-15	AF198779.1	NT	801148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
2739	5513		1.02	8.0E-15	BE261482.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 2/2
979	5994	11027	4.97	6.0E-15	AJ271736.1	NT	Homo sapiens chromosome 21 segment HS21C008
407	5444	10464	4.88	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
2686	7644	12759	1.12	5.0E-15	U91328.1	NT	Homo sapiens chromosome 21 segment HS21C103
424	6082	10066	2.43	4.0E-15	AL163303.2	NT	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to
4056	9090		7.1	3.0E-15	N89452.1	EST_HUMAN	ANF(CARDIODILATIN)
4770	9764		2.28	3.0E-15	P92485	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5
						NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
248	5308	10319	2.86	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
367	5416	10429	2.77	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
367	5418	10430	2.77	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
						EST_HUMAN	h108g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29.b3
2311	7286	12406	1.11	2.0E-15	BE350127.1	EST_HUMAN	MER29 repetitive element;
2311	7286	12407	1.11	2.0E-15	BE350127.1	EST_HUMAN	MER29 repetitive element;
						NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3430	8438	13464	0.91	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3430	8438	13465	0.91	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
						EST_HUMAN	xp26h01.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741521 3' similar to contains L1.13 L1
3954	8952	13942	1.02	2.0E-15	AW238499.1	EST_HUMAN	repetitive element;
4489	9479		2.55	2.0E-15	A1806335.1	EST_HUMAN	wf07706.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q61043
2702	7659		1.94	1.0E-15	A1889984.1	EST_HUMAN	Q61043 NINEIN;
2843	7662	12982	1.78	1.0E-15	BE043684.1	EST_HUMAN	b26h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539
						EST_HUMAN	MARINER TRANSPOSASE;
						EST_HUMAN	h140e02.y1 NCI_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2999182 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3787	8800		2.95	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1431	6428		1.93	7.0E-17	6763097	NT	Mus musculus epdipoprotein B editing complex 2 (Apobec2), mRNA
203	5287	10281	5.89	6.0E-17	AW983880.1	EST_HUMAN	RC1-HN0003-220300-021-504 HN0003 Homo sapiens cDNA
418	5076	10060	2.71	5.0E-17	T64110.1	EST_HUMAN	yc05h08.r1 Stragelene lung (#937210) Homo sapiens cDNA clone IMAGE:79839 5'
3550	8557	13564	0.94	4.0E-17	AA643697.1	EST_HUMAN	ni96e05.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058528 3'
2041	7023	12133	1.06	3.0E-17	AW119123.1	EST_HUMAN	xd89c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3'
3121	8137		1.31	3.0E-17	P36410	SWISSPROT	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3557	8564	13570	1.36	3.0E-17	BE328522.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
3557	8564	13571	1.36	3.0E-17	BE328522.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
351	5403	10413	2.52	2.0E-17	AI270080.1	EST_HUMAN	qf63a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
352	6403	10413	2.83	2.0E-17	AI270080.1	EST_HUMAN	qf63a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
973	5989		2.23	2.0E-17	AA722832.1	EST_HUMAN	zg81d04.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:398751 3'
2379	7351	12471	1.92	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2379	7351	12472	1.92	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2859	7879	12897	6.43	2.0E-17	P12036	SWISSPROT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDa NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
3693	8697		4.37	2.0E-17	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein, >
741	5784	10789	3.03	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1670	5666		0.97	1.0E-17	AJ271736.1	NT	Homo sapiens Xq1 pseudautosomal region; segment 2/2
1730	6725	11803	4.26	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C067
2057	7039	12148	1.51	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2274	7250	12367	2.06	1.0E-17	U79410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3488	8498		1.05	1.0E-17	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4015	9011		8.44	1.0E-17	R09942.1	EST_HUMAN	y30607.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128388 5'
3698	8702	13705	1.84	8.0E-18	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
347	5399	10407	65.43	7.0E-18	AW316976.1	EST_HUMAN	xt10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
347	5399	10408	65.43	7.0E-18	AW316976.1	EST_HUMAN	xt10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3221	8236	13257	1.08	6.0E-18	X71791.2	NT	Rattus norvegicus partial Gdn/Pn-1 gene for glia-derived nexin/protease nexin I, enhancer region
4603	9591		4.28	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYL TRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
1130	6135	11166	11.59	5.0E-18	A1280214.1	EST_HUMAN	qm65g11.x1 Soares_placenta_8to9weeks_2NbHP803W Homo sapiens cDNA clone IMAGE:1893688 3' similar to contains Alu repetitive element;
125	5193	10206	1.37	4.0E-18	BE044076.1	EST_HUMAN	h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element;
125	5193	10207	1.37	4.0E-18	BE044078.1	EST_HUMAN	h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element;
1678	8674	11749	21.73	4.0E-18	AA821814.1	EST_HUMAN	h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326
2138	7118	12232	0.98	4.0E-18	Q06430	SWISSPROT	h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326
2138	7118	12233	0.98	4.0E-18	Q06430	SWISSPROT	h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326
839	5858	10899	34.38	3.0E-18	AA814196.1	EST_HUMAN	h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326
917	5933	10987	3.2	3.0E-18	BE088634.1	EST_HUMAN	h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326
3846	8848	13856	1.1	3.0E-18	AL163247.2	NT	h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326
249	5309	10320	4.3	2.0E-18	AW838820.1	EST_HUMAN	h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326
1135	6140	13078	211.43	2.0E-18	BE256097.1	EST_HUMAN	h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326
3050	8067	13078	0.93	2.0E-18	Q39575	SWISSPROT	h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326
4291	9283		0.87	1.0E-18	T85406.1	EST_HUMAN	h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326
541	5576	10582	5.62	9.0E-18	AA281961.1	EST_HUMAN	h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326
542	5576	10582	3.19	9.0E-18	AA281961.1	EST_HUMAN	h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326
1031	5041		1.33	8.0E-18	AW974902.1	EST_HUMAN	h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326
2184	7163	12283	1.86	7.0E-18		NT	h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326
3692	8596		1.56	6.0E-18	AW852930.1	EST_HUMAN	h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326
4339	9330	14314	1.45	6.0E-18	P34986	SWISSPROT	h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326
4339	9330	14315	1.45	6.0E-18	P34986	SWISSPROT	h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 h36h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4655	9840		1.38	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4865	9845	14820	1.45	6.0E-19	AL120817.1	EST_HUMAN	DKFZp762F192_r1 762 (synonym: hma2) Homo sapiens cDNA clone DKFZp762F192 5'
550	5584	10588	0.91	4.0E-19	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2611	7573	12687	1.1	4.0E-19	BF697362.1	EST_HUMAN	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5'
3762	8765	13767	0.98	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3762	8765	13768	0.98	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4163	9158	14144	1.07	3.0E-19	Q43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4163	9158	14145	1.07	3.0E-19	Q43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4324	9316	14288	1.25	3.0E-19	AV708136.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5'
2489	7457	12572	24.97	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4323	9315		1.37	2.0E-19	AJ311783.1	EST_HUMAN	q091602.x1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69386
478	5515		1.56	1.0E-19	BE408611.1	EST_HUMAN	POLYU1 GENE
2100	7081	12196	1.18	1.0E-19	H30795.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
2645	7605		2.01	1.0E-19	D38044.1	NT	yo79g07.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains
2774	7795		5.45	1.0E-19	4758977	NT	MER10 repetitive element ;
3317	8327	13348	1.46	1.0E-19	AA834967.1	EST_HUMAN	Human gene for Ah-receptor, exon 7-9
3202	8217	13240	0.74	7.0E-20	BF328455.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3478	8486	13505	3.52	8.0E-20	P39188	SWISSPROT	aj49b12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12
4150	9145	14129	2.85	6.0E-20	BE622434.1	EST_HUMAN	MER37 repetitive element ;
4464	9454		1.02	5.0E-20	AV725123.1	EST_HUMAN	PM4-AN0096-050900-003-a04 AN0096 Homo sapiens cDNA
1581	6578	11642	1.44	4.0E-20	AL163247.2	NT	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
2079	7060	12170	1.22	3.0E-20	U03888.1	NT	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
4088	9082	14073	1.46	3.0E-20	P23273	SWISSPROT	AV725123 HTC Homo sapiens cDNA clone HTC8TA01 5'
4491	8481	14460	1.27	3.0E-20	AA037616.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
820	5840		48.46	2.0E-20	AW303868.1	EST_HUMAN	Human BXP21 gene
1094	6101	11130	3.05	2.0E-20	AA516335.1	EST_HUMAN	OLFATORY RECEPTOR-LIKE PROTEIN 114
1094	6101	11131	3.05	2.0E-20	AA516335.1	EST_HUMAN	z36b12.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to
							contains L1.13 L1 repetitive element ;
							x24e10.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE
							P07461 40S RIBOSOMAL PROTEIN S5 ;
							ng69h09.s1 NCL_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224068
							G1224068 ORF2: FUNCTION UNKNOWN ;
							ng69h09.s1 NCL_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066
							G1224068 ORF2: FUNCTION UNKNOWN ;

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2745	5840		36.55	2.0E-20	AW303868.1	EST_HUMAN	x24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761088.3' similar to SW:RS5_MOUSE
4789	9773	14756	4.58	2.0E-20	Q28983	SWISSPROT	P97461.40S RIBOSOMAL PROTEIN S5 ;
4789	9773	14757	4.58	2.0E-20	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
4989	9946		1.73	2.0E-20	5174538	NT	ZONADHESIN PRECURSOR
							Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
1963	7703	12051	2.7	1.0E-20	AA281961.1	EST_HUMAN	z111008.11 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811.5' similar to contains MER18.12
							MER19 repetitive element ;
4316	9308	14283	1.12	1.0E-20	BF115159.1	EST_HUMAN	tr84606.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155.3' similar to contains L1.12 L1
2842	7862		1.16	9.0E-21	AJ003514.1	EST_HUMAN	repetitive element ;
2016	6999	12102	1.61	7.0E-21	P15800	SWISSPROT	AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPI12-8J21
2016	6999	12103	1.61	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
4133	9128		6.12	7.0E-21	AA046502.1	EST_HUMAN	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
3987	8985	13971	0.98	6.0E-21	BE408611.1	EST_HUMAN	z67a06.r1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858.5'
913	5929	10964	0.79	5.0E-21	BE968839.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310.5'
4238	9232	14215	3.34	5.0E-21	BE968839.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4548	5929	10964	0.83	5.0E-21	BE968839.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4657	8842	14631	6.35	5.0E-21	4885474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
1696	6691	11767	1.66	4.0E-21	AA970713.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
1801	6792	11882	1.05	3.0E-21	AA218891.1	EST_HUMAN	0086e08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094.3' similar to TR:Q16530 Q16530
2212	7189	12310	0.99	3.0E-21	AL163201.2	NT	PMS3 MRNA ; contains OFR.11 OFR repetitive element ;
3006	8023	13035	3.56	3.0E-21	AJ007073.1	EST_HUMAN	zq15006.s1 Stragene fetal retina 837202 Homo sapiens cDNA clone IMAGE:628771.3'
145	5211		18.78	2.0E-21	BE163247.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
922	5938	10969	0.87	2.0E-21	AB007857.2	NT	Homo sapiens LGMD2B gene
1195	6199	12648	2.36	2.0E-21	BE064410.1	EST_HUMAN	QV3-HT0458-170200-090-g12 HT0458 Homo sapiens cDNA
2567	7530	12648	2.35	2.0E-21	Q28983	SWISSPROT	Homo sapiens mRNA for KIAA0397 protein, partial cds
2567	7530	12649	2.35	2.0E-21	Q28983	SWISSPROT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1236	6234	11278	1.4	1.0E-21	AA557657.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
1378	6376		10.63	1.0E-21	AI601264.1	EST_HUMAN	ZONADHESIN PRECURSOR
4286	9278	14266	1.11	9.0E-22	AI702438.1	EST_HUMAN	ZONADHESIN PRECURSOR
							nl46c04.s1 NCI_CGAP_P44 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
							MER29 repetitive element ;
							ar88d12.x1 Barstead colon HPLR87 Homo sapiens cDNA clone IMAGE:2162343.3'
							tz44a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2286204.3' similar to TR:Q16408 Q16408
							NEUTRAL PROTEASE LARGE SUBUNIT ;

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Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
834	5951		5.16	8.0E-22	BE144748.1	EST_HUMAN	CMO-HT0179-281098-076-h05 HT0179 Homo sapiens cDNA
837	5684	10691	4.6	7.0E-22	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
4160	9155	14138	2.11	7.0E-22	Q61838	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
4872	9851	14826	0.98	7.0E-22	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3551	8556		13.85	4.0E-22	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
944	5961		0.98	3.0E-22	AI469879.1	EST_HUMAN	Im14h10.x1 NCI_CGAP_Col4 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gb:1.18593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN); contains L1.t1 L1 repetitive element ;
2495	7463	12578	2.28	3.0E-22	AI859038.1	EST_HUMAN	wf66504.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2429839 3' similar to SW:RL21_HUMAN
3588	8595		1.25	3.0E-22	D14718.1	NT	P46778 60S RIBOSOMAL PROTEIN L21 ;
4856	8941	14630	3.17	3.0E-22	AI090125.1	EST_HUMAN	Human chromosome 17p11.2-p11.1 related gene
1913	6899		2.09	2.0E-22	N24942.1	EST_HUMAN	q28c07.x1 Soares pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to contains MER12.12 MER12 repetitive element ;
2452	7422	12537	1.44	2.0E-22	P24916	SWISSPROT	yx73d05.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:267369 3'
3335	8345	13363	3.8	2.0E-22	8394043	NT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
4104	9098	14084	1.53	2.0E-22	AW817794.1	EST_HUMAN	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
1840	6830	11919	1.41	1.0E-22	AW865517.1	EST_HUMAN	PM1-ST0262-261189-001-412 ST0262 Homo sapiens cDNA
2507	7475	12590	1.47	1.0E-22	U50871.1	NT	PM4-SN0020-010400-009-h02 SN0020 Homo sapiens cDNA
3326	8336	13356	1.7	1.0E-22	D14547.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
3238	8251		2.43	7.0E-23	AV647246.1	EST_HUMAN	Human DNA, SINE repetitive element
3349	8358		1.59	6.0E-23	AF199333.1	NT	AV647248 GLC Homo sapiens cDNA clone GLCAW C07 3'
4146	9141	14125	1.04	6.0E-23	AL163249.2	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
5055	8358		1.07	6.0E-23	AF199333.1	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
658	5685	10892	3.39	2.0E-23	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1125	7697		3.75	2.0E-23	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
2723	7680	12763	1.37	2.0E-23	P22105	SWISSPROT	HUMAN matrix Gla protein (MGP) gene, complete cds
2723	7680	12764	1.37	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3289	8300		1.07	2.0E-23	AI201458.1	EST_HUMAN	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3634	8640		4.12	2.0E-23	BE165980.1	EST_HUMAN	qs3f11.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537
3859	8870	13874	2.39	2.0E-23	H59931.1	EST_HUMAN	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
3859	8870	13875	2.39	2.0E-23	H59931.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
4397	9388	14371	1.16	1.0E-23	AL163252.2	NT	yt16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
4620	8605		4.78	1.0E-23	AL163210.2	NT	yt16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'

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Table 4
Single Exon Probes Expressed in HBL100 Cells

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1542	6640	11597	1.66	7.0E-26	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3873	8874	13879	1.32	7.0E-26	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
4035	9031	14018	1.76	7.0E-26	AW340153.1	EST_HUMAN	h02e12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908366 3'
2164	7143	12261	9.02	6.0E-26	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
3271	8283	13306	1.78	6.0E-26	AA208131.1	EST_HUMAN	z052h04.r1 Stratagene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:645271 5'
1158	6162	11196	5.17	5.0E-26	AI708235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371
1158	6162	11197	5.17	5.0E-26	AI708235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371
1721	6716	11792	1.25	3.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
1881	6966		2.26	3.0E-26	AA115895.1	EST_HUMAN	z030d08.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3691	8695	13697	1.2	3.0E-26	AA152464.1	EST_HUMAN	z030f10.r1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
3691	8695	13698	1.2	3.0E-26	AA152464.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR
673	5688	10707	5.99	2.0E-26	AL163282.2	EST_HUMAN	z030f10.r1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
1831	8821	13199	2.34	2.0E-26	X86694.1	NT	G695374 THYROID RECEPTOR INTERACTOR
3160	8176	10218	5.27	1.0E-26	BE170371.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
137	5203	10218	58.33	1.0E-26	BE170371.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
2492	7460	12575	1.04	1.0E-26	BE14995.1	EST_HUMAN	DKFZp566L171_s1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566L171 3'
2615	7577		57.21	1.0E-26	AF261085.1	NT	Musculus mRNA for astrocytic phosphoprotein, FEA-15
11	5091	10075	2.7	8.0E-27	AI831462.1	EST_HUMAN	QV4-HT0538-020300-123-a02 HT0538 Homo sapiens cDNA
553	5587		2.73	8.0E-27	AL163227.2	NT	MR2-BND114-240500-030-g07 BND114 Homo sapiens cDNA
1391	6388	11440	83.09	8.0E-27	AW162737.1	EST_HUMAN	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds
1391	6388	11441	83.09	8.0E-27	AW162737.1	EST_HUMAN	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds
2103	7083	12188	1.71	8.0E-27	AW884776.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2
3111	8127	13147	2.66	8.0E-27	P12236	SWISSPROT	THR repetitive element
							Homo sapiens chromosome 21 segment HS21C027
							Homo sapiens chromosome 21 segment HS21C027
							au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558
							TUBULIN ALPHA-1 CHAIN (HUMAN)
							au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558
							TUBULIN ALPHA-1 CHAIN (HUMAN)
							PM2-SN0018-220300-002-a07 SN0018 Homo sapiens cDNA
							ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE
							NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
675	5700		1.35	7.0E-27	Z70684.1	NT	Human endogenous retroviral element HC2
4918	9896		2.5	7.0E-27	AW629172.1	EST_HUMAN	h151h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040
1990	6975	12080	2.62	3.0E-27	X60698.1	NT	O76040 ORF2: FUNCTION UNKNOWN. ; R. ratus RYA3 mRNA for a potential ligand-binding protein
4149	9144	14128	1.26	3.0E-27	BE071924.1	EST_HUMAN	PMD-BT0527-090100-001-411 BT0527 Homo sapiens cDNA
42	5122	10110	36.88	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1855	6844		37.38	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.s1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
3036	8053		10.93	2.0E-27	AW629172.1	EST_HUMAN	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); h151h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040
3153	8169	13189	1.99	2.0E-27	AF111167.2	NT	O76040 ORF2: FUNCTION UNKNOWN. ;
3153	8169	13189	1.99	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
433	6471		1.55	1.0E-27	AL163246.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
981	5996	11028	1.2	1.0E-27	AB026886.1	NT	Homo sapiens chromosome 21 segment HS21C046
3966	8964		1.02	1.0E-27	BE350127.1	EST_HUMAN	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
141	5208		2.16	9.0E-28	BE346399.1	EST_HUMAN	h109g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MIER29.b3
309	6364	10375	2.37	9.0E-28	AU126280.1	EST_HUMAN	MER29 repetitive element ;
1162	6166	11200	15.2	7.0E-28	AU142750.1	EST_HUMAN	h1w17c11.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
316	5371		2.32	5.0E-28	AI921003.1	EST_HUMAN	SECRETED NEUREXIN III-ALPHA-C PRECURSOR. [3] TR:Q07280 TR:Q07313 ;
3902	8902	13900	1.66	5.0E-28	R79782.1	EST_HUMAN	AU126260 NT2RP1 Homo sapiens cDNA clone NT2RP1000443 5'
2552	7517	12635	2.12	4.0E-28	AW195088.1	EST_HUMAN	AU142750 Y79AA1 Homo sapiens cDNA clone Y79AA1000824 5'
2908	7927	12945	1.09	4.0E-28	4505316	NT	wo18c07.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2456692 3' similar to contains THR.b1
3035	8052	13091	5.95	4.0E-28	BE409100.1	EST_HUMAN	THR repetitive element ;
1264	6262		1.68	3.0E-28	AF155382.1	NT	y89f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146443 5'
87	6164	10175	8.92	2.0E-28	BE062167.1	EST_HUMAN	xn33c09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695504 3' similar to SW:GG95_HUMAN
1147	6151	11183	10.35	2.0E-28	Y11107.3	NT	Q08379 GOLGIN-95. ; Q08379 GOLGIN-95. ; Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
							601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635305 5'
							Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
							Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
							RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA
							Homo sapiens ITG94 gene for integrin beta 4 subunit, exons 3-41

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2405	7378	12496	1.68	2.0E-28	A1348634.1	EST_HUMAN	q035806.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1810483 3' similar to contains L1.b2 L1
3281	8293	13318	0.68	2.0E-28	AL163209.2	NT	repetitive element; Homo sapiens chromosome 21 segment HS21C008
1448	6445	11504	1.71	1.0E-28	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2168	7137	12256	2.04	1.0E-28	BF333238.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
4436	9426		2.22	1.0E-28	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
5003	9974	14949	1.55	1.0E-28	P23275	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)
1567	6564	11627	1.17	7.0E-29	AW988447.1	EST_HUMAN	EST378521 IMAGE resequences, MAGI Homo sapiens cDNA
3476	8484		1.34	7.0E-28	BE254708.1	EST_HUMAN	601114980F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475
590	5621	10620	9.68	6.0E-29	A1936748.1	EST_HUMAN	wp69b01.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15475
4839	8823		1.37	5.0E-28	AL163203.2	NT	O15475 UNNAMED HERV-H PROTEIN ; contains LTR7.b1 LTR7 repetitive element ;
3161	8177		1.75	4.0E-29	A1752367.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
4290	9282	14270	1.28	3.0E-29	AB042287.1	NT	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
489	5525	10532	1.15	2.0E-28	AF084869.1	NT	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
489	5525	10533	1.15	2.0E-28	AF084869.1	NT	Hom sapiens PTS gene for 6-pyruvyltetrahydropterin synthase, complete cds
1501	6499	11553	4.66	2.0E-29	A1963604.1	EST_HUMAN	Hom sapiens envelope protein RIC-8 (env) gene, complete cds
1501	6499	11554	4.66	2.0E-29	A1963604.1	EST_HUMAN	Hom sapiens envelope protein RIC-8 (env) gene, complete cds
4157	9152	14134	2.09	2.0E-28	AL163268.2	NT	Hom sapiens envelope protein RIC-8 (env) gene, complete cds
1484	6481		1.34	7.0E-30	BE091133.1	EST_HUMAN	Hom sapiens envelope protein RIC-8 (env) gene, complete cds
1534	6532		0.9	6.0E-30	X51755.1	NT	HERV-E ENVELOPE GLYCOPROTEIN ;
1736	6731	11808	1.1	6.0E-30	D25303.1	EST_HUMAN	HERV-E ENVELOPE GLYCOPROTEIN ;
3117	8133	13152	2.42	6.0E-30	BE008026.1	EST_HUMAN	HERV-E ENVELOPE GLYCOPROTEIN ;
4614	8133	13152	0.93	6.0E-30	BE008026.1	EST_HUMAN	HERV-E ENVELOPE GLYCOPROTEIN ;
3906	8906	13904	40.12	5.0E-30	A1399992.1	EST_HUMAN	HERV-E ENVELOPE GLYCOPROTEIN ;
2082	7063	12172	1.93	4.0E-30	AW637471.1	EST_HUMAN	HERV-E ENVELOPE GLYCOPROTEIN ;
2082	7063	12173	1.93	4.0E-30	AW637471.1	EST_HUMAN	HERV-E ENVELOPE GLYCOPROTEIN ;
1134	6139		3.35	3.0E-30	A1338551.1	EST_HUMAN	HERV-E ENVELOPE GLYCOPROTEIN ;
3672	8677	13680	0.82	3.0E-30	AF128893.1	NT	HERV-E ENVELOPE GLYCOPROTEIN ;

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
667	5682	10701	1.21	2.0E-30	AW857315.1	EST_HUMAN	CMO-CT0307-310100-158-H03 CT0307 Homo sapiens cDNA
1068	6076		2.48	2.0E-30	F08698.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
1449	6446	11505	8.55	2.0E-30	BE176877.1	EST_HUMAN	RC5-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA
2843	7803	12716	6.5	2.0E-30	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
2849	7869	12885	6.88	2.0E-30	AF114156.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
3700	8704	13707	2.23	2.0E-30	AW206581.1	EST_HUMAN	UI-H-B11-af-c-12-0-LJ1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722598 3'
4833	9618	14609	1.61	2.0E-30	BE288945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
4833	9618	14610	1.81	2.0E-30	BE288945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
284	5342	10355	13.84	1.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (Tfujwara) Homo sapiens cDNA clone GEN-570C01 5'
533	5568	10571	3.42	1.0E-30	AW468897.1	EST_HUMAN	hd30504.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains
708	5730	10746	3.15	1.0E-30	AL163203.2	NT	MER1.13 MER1 MER1 repetitive element;
2150	7129	12246	2.78	1.0E-30	AA694377.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
2393	7364	12486	1.95	1.0E-30	BF347728.1	EST_HUMAN	ac77808.s1 Stragelene lung (#937210) Homo sapiens cDNA clone IMAGE:868589 3'
2880	7998	13011	0.79	1.0E-30	AA315045.1	EST_HUMAN	602022560F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157891 5'
1080	6069	11100	6.71	8.0E-31	8923389	NT	EST188668 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end
2347	7321		23.47	8.0E-31	AL163208.2	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
4763	9747	14733	1.01	8.0E-31	P23275	SWISSPROT	Homo sapiens chromosome 21 segment HS21C008
4763	9747	14734	1.01	8.0E-31	P23276	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)
701	5725		2.43	7.0E-31	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
2597	7559	12675	2.15	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2597	7559	12676	2.15	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
3594	8601		2.5	6.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
192	5256	10268	3.17	5.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 1
192	5256	10269	3.17	5.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 1
591	5622		3.18	4.0E-31	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1782	6774		1.4	4.0E-31	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2716	7673		1.63	4.0E-31	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
2519	7486	12804	1.54	3.0E-31	6005871	NT	Homo sapiens SEC83, endoplasmic reticulum translocan component (S. cerevisiae) like (SEC63L), mRNA
1873	6862	11951	2.35	2.0E-31	AW838171.1	EST_HUMAN	QV2-LT0051-260300-111-403 LT0051 Homo sapiens cDNA
2152	7131	12248	1.01	2.0E-31	AI393388.1	EST_HUMAN	ig44g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111672 3'
2278	7254	12373	1.52	2.0E-31	AL119245.1	EST_HUMAN	DKFZp761G1513_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G1513 5'

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2373	7345	12465	4.03	2.0E-31	AA468824.1	EST_HUMAN	aa88f1.81 Stratagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR12 THR repetitive element ;
15	5095	10079	10.14	1.0E-31	U93163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
1623	6620	11886	9.05	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1623	6620	11887	9.05	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1623	6620	11888	9.05	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
4501	9491	14467	1.26	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235_1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547B235 5'
4501	9491	14468	1.26	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235_1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547B235 5'
4501	9491	14468	1.26	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235_1 547 (synonym: hfbt1) Homo sapiens cDNA clone IMAGE:1675384 3'
2024	7007	12113	5.49	8.0E-32	AI056770.1	EST_HUMAN	oz15a09.x1 Soares fetal_liver_spleen_1NLS_S1 Homo sapiens cDNA clone IMAGE:1675384 3'
1017	6027	11057	84.69	5.0E-32	AF116627.1	NT	Homo sapiens PRO1181 mRNA, complete cds
918	5934		1.7	4.0E-32	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
453	5490	10505	2.46	3.0E-32	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1427	6424	11483	57.22	3.0E-32	AV731500.1	EST_HUMAN	AV731500 HTF Homo sapiens cDNA clone HTFAK07 5'
2604	7566		1.49	1.0E-32	D84430.1	NT	Homo sapiens mRNA for phenylalanyl tRNA synthetase, complete cds
3020	8037		1.65	1.0E-32	BE743299.1	EST_HUMAN	601573207F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834433 5'
							hw07c05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:O88539 O88539 WW DOMAIN BINDING PROTEIN 11 ;
3400	8409		5.22	9.0E-33	BE327112.1	EST_HUMAN	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
62	5142	10144	11.74	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
62	5142	10145	11.74	7.0E-33	5031736	NT	hs12b09.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178909 3' similar to contains OFR.11 OFR repetitive element ;
2097	7078	12192	1.93	7.0E-33	AI590115.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5'
2576	7539		7.4	7.0E-33	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5'
2757	6655	11727	1.01	7.0E-33	AV730015.1	EST_HUMAN	AV730015 HTF Homo sapiens cDNA clone HTFAVE06 5'
3168	8184		14.85	7.0E-33	AW971307.1	EST_HUMAN	EST383398 IMAGE resequences, MAGL Homo sapiens cDNA
3652	8658		0.8	6.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1740	6735		1.43	5.0E-33	BF373151.1	EST_HUMAN	QV1-FT0169-100700-271-802 FT0169 Homo sapiens cDNA
1842	6832		0.97	5.0E-33	11141884	NT	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC6A7), mRNA
1858	6847	11934	4.15	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1858	6847	11935	4.15	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
2210	7187		1.61	5.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
3945	8943	13933	1.87	5.0E-33	AB014599.1	NT	Homo sapiens mRNA for KIAA0699 protein, partial cds
5065	10034	15001	1.07	5.0E-33	M64350.1	NT	Human TCR variable region Va30 subfamily gene (VA30, JA, CA segments), 5' end
1111	6117		1.87	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2668	7048	12156	1.97	4.0E-33	4758987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2353	7327		1.14	4.0E-33	AA626621.1	EST_HUMAN	ab51b11.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28.b2/MER28 repetitive element ;
2474	7443	12558	2.2	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4356	9347	14327	1.46	4.0E-33	AW293349.1	EST_HUMAN	U1-H-B12-ah1-c-03-Q-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
1073	6081		5.08	3.0E-33	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
1074	6081		3.82	3.0E-33	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
2382	7770		1.73	3.0E-33	AV847851.1	EST_HUMAN	AV847851 GLC Homo sapiens cDNA clone GLOC0909 3'
18	5098		1.02	2.0E-33	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFR repetitive element ;
105	5096		2.37	2.0E-33	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFR repetitive element ;
4295	9287		5.1	2.0E-33	BE159039.1	EST_HUMAN	MRO-H10405-160300-202-008 HT0405 Homo sapiens cDNA
4828	9810	14791	30.71	2.0E-33	AA626883.1	EST_HUMAN	ab51g11.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb:X00734 cds1 TUBULIN BETA-5 CHAIN (HUMAN);
4922	9900	14875	2.2	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
4922	9900	14876	2.2	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
9	5089		1.61	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4368	9360	14340	1.09	8.0E-34	BE062570.1	EST_HUMAN	QV2-BT0258-071299-019-g07 BT0258 Homo sapiens cDNA
1419	6416	11476	2.31	7.0E-34	T70845.1	EST_HUMAN	yd15a05.r1 Soares_fetal_liver_spleen_1N1FLS Homo sapiens cDNA clone IMAGE:108320 5'
468	5504	10517	1.48	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
468	5504	10518	1.48	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
1841	6831		2.53	5.0E-34	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
4893	9872	14839	5.04	5.0E-34	U30883.1	NT	Human splicing factor SRP55-1 (SRP-55) mRNA, complete cds
1952	6938	12040	1.38	4.0E-34	AI804667.1	EST_HUMAN	h94c08.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2249194 3'
2647	7607	12719	0.82	4.0E-34	8922807	NT	Homo sapiens hypothetical protein FLJ10989 (FLJ10989), mRNA
3099	8115	13133	1.38	4.0E-34	5903166	NT	Homo sapiens splicing factor 3a, subunit 3, 60kD (SF3A3), mRNA
1475	6472	11530	14.56	1.0E-34	P12236	SWISSPROT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3589	8586	13600	1.32	1.0E-34	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3957	8955	13944	0.83	1.0E-34	AY008937.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
3957	8955	13945	0.83	1.0E-34	AY008937.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4352	9343		4.5	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0506-240400-016-h08 BT0506 Homo sapiens cDNA
3560	8567	13573	1.41	9.0E-35	AW663302.1	EST_HUMAN	hh7b06.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988787 5'
224	5286		25.01	8.0E-35	6031190	NT	Homo sapiens prohibitin (PHB) mRNA
1699	6694	11770	2.3	8.0E-35	BF589937.1	EST_HUMAN	naa33a08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:075912
1699	6694	11771	2.3	8.0E-35	BF589937.1	EST_HUMAN	naa33a08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:075912
4717	9702	14688	3.04	8.0E-35	BF183195.1	EST_HUMAN	075912 DIACYLGLYCEROL KINASE IOTA ;
1388	6385	11437	1.5	6.0E-35	AA757115.1	EST_HUMAN	601809588F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 5'
1925	6911	12006	1.65	6.0E-35	6005975	NT	ah5h03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1309397 3'
5063	10032		0.75	6.0E-35	8923389	NT	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
1671	6667	11742	1.53	5.0E-35	X63392.1	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
2711	7668	12781	1.05	5.0E-35	AB007866.2	NT	H. sapiens immunoglobulin kappa light chain variable region L14
2939	7959	12977	1.22	5.0E-35	6912639	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
							Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
							Homo sapiens cdk2 kinase (CLK2), prolin1, cote1, glucocerebrosidase (GBA), and metaxin genes, complete cds; metaxin pseudogene and glucocerebrosidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds
4285	9277	14285	1.3	5.0E-35	AF023268.1	NT	cds
1408	6406	11465	66.29	4.0E-35	BE257907.1	EST_HUMAN	601109719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'
							y498a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element ;
1783	6775	11866	19.99	4.0E-35	H91193.1	EST_HUMAN	601125260F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'
1544	6542	11600	52.74	3.0E-35	BE268182.1	EST_HUMAN	Homo sapiens phospholipid scramblase 1 gene, complete cds
2269	7246		1.68	3.0E-35	AF224492.1	NT	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
108	7713	10192	1.21	2.0E-35	N88965.1	EST_HUMAN	A971F Heart Homo sapiens cDNA clone A971
1188	6171	11206	1.09	2.0E-35	T11909.1	EST_HUMAN	Homo sapiens mRNA for Gab2, complete cds
2156	7135	12254	2.74	2.0E-35	AB018413.1	NT	hi86a12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979166 3' similar to SW:TR12_HUMAN Q14669 THYROID RECEPTOR INTERACTING PROTEIN 12 ;
2612	7574	12688	1.92	2.0E-35	AW665005.1	EST_HUMAN	Homo sapiens mRNA for KIAA0895 protein, partial cds
3490	8498		0.84	2.0E-35	AB020702.1	NT	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
3814	8817	13823	0.81	2.0E-35	BE247575.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3814	8817	13824	0.81	2.0E-35	BE247576.1	EST_HUMAN	TCBAP2E-4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
4535	9525		2.63	2.0E-35	H49239.1	EST_HUMAN	y19a12.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:274079 5'
47	5128	10119	6.23	1.0E-35	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
47	5128	10120	6.23	1.0E-35	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
743	5766	10780	140.65	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-008-412 ST0162 Homo sapiens cDNA
743	5766	10781	140.65	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-008-412 ST0162 Homo sapiens cDNA
898	5916		1.2	1.0E-35	T87947.1	EST_HUMAN	y493a01.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to SP-A44282 A44282 RETROVIRUS-RELATED POL POLYPROTEIN - HUMAN ;
2471	7439	12555	2.17	1.0E-35	7705994	NT	Homo sapiens hypothetical protein (LOC51233), mRNA
2694	7652	12786	1.37	1.0E-35	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29.B3
2694	7652	12787	1.37	1.0E-35	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29.B3
2894	8086	13100	1.24	1.0E-35	6006030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
3090	8106	13121	2.49	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEP08 3'
3090	8106	13122	2.49	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEP08 3'
4298	9280	14276	4.67	1.0E-35	7656905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
4298	9280	14277	4.67	1.0E-35	7656905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
3879	8880	13883	1.75	9.0E-36	AW821707.1	EST_HUMAN	RC3-ST0315-180200-013-412 ST0315 Homo sapiens cDNA
2860	7880	12898	2.3	7.0E-36	AW857579.1	EST_HUMAN	GM1-CT0315-091298-063-407 CT0315 Homo sapiens cDNA
3044	8061		4.78	7.0E-36	4657498	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
1957	6943	12045	1.89	6.0E-36	7706622	NT	Homo sapiens nirxurin 2 (NINJ2), mRNA
2351	7325		6.02	6.0E-36	AB036346.1	NT	Homo sapiens TCEB1 gene, exon 12
3554	8561	13567	1.16	6.0E-36	BF515101.1	EST_HUMAN	UI-H-BW1-ant-c-12-q-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
138	5204	10219	10.77	5.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2678	7636	12751	24.76	5.0E-36	BE388436.1	EST_HUMAN	601285557F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'
3531	8537	13542	1.37	5.0E-36	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4843	9828	14621	2.22	5.0E-36	5729729	NT	Homo sapiens API5-like 1 (API5L1), mRNA
4843	9828	14622	2.22	5.0E-36	5729729	NT	Homo sapiens API5-like 1 (API5L1), mRNA
1205	6206	11243	2.05	4.0E-36	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1416	6413	11474	1.38	4.0E-36	P10266	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
1606	6602	11664	1.78	4.0E-36	BE382574.1	EST_HUMAN	ENDONUCLEASE
							601288574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628388 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2161	7140		4.99	4.0E-36	AW247772.1	EST_HUMAN	2820020.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3276	8287	13311	0.88	4.0E-36	BE389289.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
3275	8287	13312	0.98	4.0E-36	BE389289.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
687	5711	10725	2.91	3.0E-36	AF098810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
1488	6485	11524	1.3	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
1488	6485	11525	1.3	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
2235	7212	12329	2.14	3.0E-36	7862401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
4373	9365	14345	6.39	3.0E-36	10181139	NT	Mus musculus juncatophilin 1 (Jp1-pending), mRNA
3086	8112	13130	6.65	2.0E-36	BE259267.1	EST_HUMAN	601106343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342706 5'
4802	9786	14788	17.98	2.0E-36	AW880376.1	EST_HUMAN	QV0-Q70030-240300-174-H04 OT0030 Homo sapiens cDNA
874	5892	10633	1.87	1.0E-36	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2084	7085	12176	1.85	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131189-021-H07 HT0217 Homo sapiens cDNA
2084	7085	12177	1.85	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131189-021-H07 HT0217 Homo sapiens cDNA
2139	7119	12234	1.5	1.0E-36	BF673761.1	EST_HUMAN	602136483F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 5'
3269	8282		1.42	1.0E-36	AF158862.1	NT	Homo sapiens human endogenous retrovirus W proC8-19 protease (pro) gene, partial cds
3276	8288	13313	0.98	8.0E-37	4757979	NT	Homo sapiens chimerin (chimaerin) 2 (CHN2), mRNA
1265	6263		2.68	7.0E-37	AL042800.1	EST_HUMAN	DKFZp434E0422_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0422 5'
1705	6700	11776	1.1	7.0E-37	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
1705	6700	11777	1.1	7.0E-37	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4955	9932		1.57	6.0E-37	R10039.1	EST_HUMAN	yf25a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127850 5'
2357	7331	12447	2.14	4.0E-37	AA702784.1	EST_HUMAN	z180b04.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
5038	10009		0.81	4.0E-37	N62051.1	EST_HUMAN	EST52g10 WATM1 Homo sapiens cDNA clone 52g10 similar to human STS G04101
1987	6952	12056	1.95	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
1987	6952	12057	1.95	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
2441	7411		1.2	3.0E-37	AW981150.1	EST_HUMAN	EST7373222 MAGF resequences, MAGF Homo sapiens cDNA
2895	7914		3.82	3.0E-37	AW981150.1	EST_HUMAN	EST7373222 MAGF resequences, MAGF Homo sapiens cDNA
4831	9815		0.76	3.0E-37	BF035327.1	EST_HUMAN	601458331F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3662088 5'
380	5455	10472	1.71	2.0E-37	D89790.1	NT	Homo sapiens mRNA for AML1, complete cds
380	5455	10473	1.71	2.0E-37	D89790.1	NT	Homo sapiens mRNA for AML1, complete cds
1084	6072	11104	2.16	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1064	6072	11105	2.16	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
1923	6909	12004	1.45	2.0E-37	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
3798	8801	13808	4.94	2.0E-37	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
4123	9118	14104	0.78	2.0E-37	4826685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
2034	7017	12127	3.59	1.0E-37	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
3124	8140		0.98	1.0E-37	AW862082.1	EST_HUMAN	RC3-CT0347-210400-016-h03 CT0347 Homo sapiens cDNA
3855	8857	13863	1.18	1.0E-37	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4783	9787	14751	2.02	1.0E-37	BF371719.1	EST_HUMAN	QV0-FN0180-280700-318-ct0 FN0180 Homo sapiens cDNA
1202	6203	11240	1.69	8.0E-38	11436955	NT	Homo sapiens Gb2-associated binder 2 (KIAA0571), mRNA
2425	7396	12517	1.23	8.0E-38	BF346221.1	EST_HUMAN	602018401F1 NC1 CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153992 5'
2119	7099	12212	5.28	7.0E-38	AW972825.1	EST_HUMAN	EST384920 MAGC resequences, MAGL Homo sapiens cDNA
2869	7987	13001	2.99	6.0E-38	BF033033.1	EST_HUMAN	601455722F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3659348 5'
717	5740	10757	1.86	5.0E-38	AW971819.1	EST_HUMAN	EST389308 MAGC resequences, MAGL Homo sapiens cDNA
2395	7356	12478	4.11	5.0E-38	AJ237740.1	NT	Homo sapiens RIBIR gene (partial), exon 8
4991	7356	12478	1.09	5.0E-38	AJ237740.1	NT	Homo sapiens RIBIR gene (partial), exon 8
119	5189	10200	3.97	4.0E-38	Z25466.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
119	5189	10201	3.97	4.0E-38	Z25466.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
2043	7025		2.4	3.0E-38	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3613	8620		1.58	3.0E-38	7549807	NT	Homo sapiens HIRA interacting protein 4 (dha1-like) (HIRIP4), mRNA
3765	8768	13772	1.58	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
3765	8768	13773	1.58	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
4482	9472		1.26	3.0E-38	BE279301.1	EST_HUMAN	601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'
51	5132	10127	1.71	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1361	6358	11408	8.04	2.0E-38	5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
1607	6603	11665	1.7	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
1607	6603	11666	1.7	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
3455	8463		0.91	2.0E-38	AF070670.1	NT	Homo sapiens protein phosphatase 2C alpha 2 mRNA, complete cds
4448	9438	14421	5	2.0E-38	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4953	9930	14909	0.75	2.0E-38	BE296224.1	EST_HUMAN	60117386F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532580 5'
4953	9930	14910	0.75	2.0E-38	BE296224.1	EST_HUMAN	60117386F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532580 5'

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1076	6083		1.97	1.0E-38	AA401570.1	EST_HUMAN	zu62502.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element
1953	6939	12041	3.28	1.0E-38	4885288	NT	MER19 repetitive element:
1970	6955	12059	0.96	1.0E-38	7661868	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
2423	7394	12515	2.9	1.0E-38	AF270831.1	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
4192	8185	14168	0.72	1.0E-38	4505016	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
4197	8190	14171	1.27	1.0E-38	AL163203.2	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4197	8190	14172	1.27	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4468	9458	14436	1.08	1.0E-38	8922543	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
55	5136	10133	6.42	8.0E-39	4502312	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA
1371	6368	11417	1.13	8.0E-39	4758229	NT	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
1793	6784		1.43	8.0E-39	AI823404.1	EST_HUMAN	wh53f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890
2038	7021	12130	4.22	7.0E-39	AL163227.2	NT	POL PROTEIN ;
992	6005	11036	1.95	5.0E-39	AF003528.1	NT	Homo sapiens chromosome 21 segment HS21C027
2816	7935	12853	6.76	5.0E-39	AI750154.1	EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
546	5580	10584	50.63	4.0E-39	AB015610.1	NT	at36b04.x1 Berstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408
3482	8500	13514	0.7	4.0E-39	AL163210.2	NT	Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ; contains LTR7.11 LTR7 repetitive element ;
48	5129	10121	18.3	3.0E-39	AA631949.1	EST_HUMAN	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
48	5129	10122	18.3	3.0E-39	AA631949.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
48	5129	10123	18.3	3.0E-39	AA631949.1	EST_HUMAN	frnfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
886	5904		18.94	2.0E-39	BE409203.1	EST_HUMAN	frnfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
901	5919		8.24	2.0E-39	AI525119.1	EST_HUMAN	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'
1015	6025		3.1	2.0E-39	AF000573.1	NT	promrna-7.D01.r bvtumor Homo sapiens cDNA 5'
1498	6488		89.79	2.0E-39	AW372318.1	EST_HUMAN	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
1929	6915	12012	2.58	2.0E-39	AA720574.1	EST_HUMAN	PMO-BT0340-211299-003-002 BT0340 Homo sapiens cDNA
2556	7521	12638	1.41	2.0E-39	AL163248.2	NT	nw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13
4278	9272	14261	1.83	2.0E-39	BF370207.1	EST_HUMAN	THR repetitive element ;
1482	6479	11535	11.08	1.0E-39	AJ006345.1	NT	Homo sapiens chromosome 21 segment HS21C048

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1482	6479	11536	11.08	1.0E-39	AJ008345.1	NT	Homo sapiens KVLQT1 gene
1499	6497	11550	4.37	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZp434P211). mRNA
4525	9515	14500	15.01	1.0E-39	AW951995.1	EST_HUMAN	EST364065 MAGE resequences, MAGE Homo sapiens cDNA
4525	9515	14501	15.01	1.0E-39	AW951995.1	EST_HUMAN	EST364065 MAGE resequences, MAGE Homo sapiens cDNA
4584	9552	14538	7.93	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZp434P211). mRNA
551	5585	10587	1.74	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2). mRNA
1215	6214	11253	11.93	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1215	6214	11254	11.93	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1423	6420	11480	1.06	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
3697	8701	13704	1.19	9.0E-40	4503764	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
3866	10048	13870	3.4	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4370	9214	14193	0.88	9.0E-40	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
2968	7886	13000	0.96	8.0E-40	AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H15A04
3823	8825		4.61	8.0E-40	BE396541.1	EST_HUMAN	601288958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619166 5'
2654	7614	12724	6.7	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to similar to zinc finger protein family
2854	7614	12725	6.7	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to similar to zinc finger protein family
2529	7495	12815	1.57	5.0E-40	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1838	6828	11917	1.77	4.0E-40	AI886005.1	EST_HUMAN	t891b01.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O73505 O73505 POL PROTEIN. ;
2050	7032		2.06	4.0E-40	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4264	9257	14247	8.89	4.0E-40	7662117	NT	Homo sapiens KIAA0433 protein (KIAA0433). mRNA
4011	9007	13968	0.99	3.0E-40	AI925949.1	EST_HUMAN	wh1207.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380549 3'
323	5377		3.68	2.0E-40	AI223036.1	EST_HUMAN	qg52h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838847 3'
786	5807		47.86	2.0E-40	AW303868.1	EST_HUMAN	x24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5. ;
1780	6781		2.37	2.0E-40	AV731601.1	EST_HUMAN	AV731601 HTF Homo sapiens cDNA clone HTFAZE05 5'
1894	6882	11973	6.41	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
1894	6882	11974	6.41	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2105	7085	12200	1.63	2.0E-40	5453592	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
2618	7580		1.3	2.0E-40	BE275932.1	EST_HUMAN	601121667F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5'
3053	8070	13080	4.08	2.0E-40	5453592	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
4745	9730	14717	1.8	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4745	9730	14718	1.8	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5005	9978	14951	1	2.0E-40	4505980	NT	Homo sapiens plasminogen (PLG) mRNA
872	5890		1.42	1.0E-40	AA225989.1	EST_HUMAN	nc09a09.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007608
2548	7613	12631	1.42	1.0E-40	BF036881.1	EST_HUMAN	601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863803 5'
							601460375F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158
							SYNTAXIN 17.
2814	7576		1.6	1.0E-40	BE018348.1	EST_HUMAN	
2863	7622	12733	0.98	1.0E-40	BF641030.1	EST_HUMAN	602088604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5'
2663	7622	12734	0.99	1.0E-40	BF641030.1	EST_HUMAN	602088604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5'
3224	8239		1.22	1.0E-40	4507142	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
4478	9488	14448	5.47	1.0E-40	4508012	NT	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
3715	8718	13720	1.02	9.0E-41	W01586.1	EST_HUMAN	zs36a02.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:284802 5'
818	7732	10874	1.8	7.0E-41	A1834364.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
818	7732	10875	1.8	7.0E-41	A1834364.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
5041	10012	14881	1.23	7.0E-41	11431114	NT	Homo sapiens hypothetical protein (FLJ10996), mRNA
278	5336	10350	2.15	8.0E-41	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
2052	7034	12148	4.09	6.0E-41	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
1768	6758	11844	1.57	5.0E-41	T62628.1	EST_HUMAN	yc03a10.s1 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:79826 3'
390	5428		1.45	4.0E-41	BE156318.1	EST_HUMAN	QV0-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
1081	6088	11117	1.03	4.0E-41	AU119344.1	EST_HUMAN	AU118344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
							ow45e06.s1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:Q00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE.; contains LTR5.b1 LTR5 repetitive element;
1385	6382	11432	10.1	4.0E-41	A1027117.1	EST_HUMAN	
							ow45e06.s1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:Q00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE.; contains LTR5.b1 LTR5 repetitive element;
1385	6382	11433	10.1	4.0E-41	A1027117.1	EST_HUMAN	
1398	6395	11450	3.73	4.0E-41	AB008681.1	NT	Homo sapiens gene for actin receptor type IIB, complete cds
							fm96c04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1
1595	6591	11652	4.42	4.0E-41	A1500406.1	EST_HUMAN	OFR repetitive element;
2818	7838	12854	3.89	4.0E-41	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2818	7838	12855	3.89	4.0E-41	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4021	9017	14004	2.21	4.0E-41	X92885.1	NT	H.sapiens DNase I hypersensitive site (HSS-3) enhancer element
833	5950	10983	1.82	3.0E-41	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
4208	9201	14183	3.05	3.0E-41	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1789	6527	11586	49.39	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
1918	6904	11898	1.61	2.0E-41	AA331940.1	EST_HUMAN	EST35818 Embryo, 8 week I Homo sapiens cDNA 5' end
2157	7136	12255	5.84	2.0E-41	D88662.1	NT	Human mRNA for KIAA0207 gene, complete cds
2206	7183	12306	15.51	2.0E-41	X89631.1	NT	G.gorilla DNA for ZNF80 gene homolog
2755	6527	11586	16.52	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
3748	8752	13751	0.8	2.0E-41	5032108	NT	Homo sapiens son of sevenless (Drosophila) homolog 1 (SOS1) mRNA
4488	9478	14458	1.15	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4488	9478	14459	1.15	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3133	8149	13170	1.16	1.0E-41	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
3133	8149	13171	1.16	1.0E-41	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
4434	8424	14409	15.19	1.0E-41	6678468	NT	Mus musculus tubulin alpha 6 (Tuba6), mRNA
460	5497	10508	5.2	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
4976	8952	14930	0.84	8.0E-42	6679031	NT	Mus musculus neural precursor cell expressed, developmentally down-regulated gene 1 (Nedd1), mRNA
919	5935		1.72	7.0E-42	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C083
1819	6809	11800	3.13	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
1819	6809	11801	3.13	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
2227	7204		2.79	6.0E-42	AW238856.1	EST_HUMAN	xp29f08.x1 NCI_CGAP_HIN10 Homo sapiens cDNA clone IMAGE:2741799 3' similar to contains L1.11 L1 repetitive element
136	5202		5.47	5.0E-42	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
435	5473	10489	1.38	5.0E-42	BE217913.1	EST_HUMAN	h37e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
483	5520		8.24	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
484	5521		3.56	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
744	5767	10792	23.3	4.0E-42	AF055066.1	NT	Homo sapiens MHC class 1 region
744	5767	10793	23.3	4.0E-42	AF055066.1	NT	Homo sapiens MHC class 1 region
1049	6058	11087	4.34	4.0E-42	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4071	9065	14055	1.98	4.0E-42	X59417.1	NT	H.sapiens PROS-27 mRNA
4106	9100	14087	0.82	4.0E-42	AF246219.1	NT	Homo sapiens SNARE protein kinase SNARE mRNA, complete cds
4127	9122	14107	4.17	4.0E-42	4506496	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA
4451	9441	14422	13.19	4.0E-42	4508008	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
104	5181		0.9	3.0E-42	AA486105.1	EST_HUMAN	ab14e10.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains
1492	6449	11510	2.61	2.0E-42	BF376834.1	EST_HUMAN	THR.12 THR repetitive element ;
2346	7320		2.82	2.0E-42	AW898344.1	EST_HUMAN	RC0-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA
2358	7332	12448	4.89	2.0E-42	AW250059.1	EST_HUMAN	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA
724	5746	10767	2.19	1.0E-42	X57147.1	NT	2819283.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819283 3'
1025	6035	11067	1.09	1.0E-42	AW265809.1	EST_HUMAN	Human endogenous retrovirus pHE.1 (ERV9)
1084	6091	11120	1.08	1.0E-42	AJ251818.1	NT	U1-H-B11-afn-e-04-Q-UJ1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1084	6091	11121	1.08	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1223	7742	11287	11.95	1.0E-42	AF087166.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1223	7742	11268	11.95	1.0E-42	AF087166.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1661	6657	11731	1.13	1.0E-42	11423219	NT	Homo sapiens NADH-ubiquinone oxidoreductase A/GGG subunit precursor homolog mRNA, nuclear gene
2473	7442	12557	1.26	1.0E-42	5174458	NT	encoding mitochondrial protein, complete cds
2894	7913	12934	5.85	1.0E-42	4505524	NT	Homo sapiens NADH-ubiquinone oxidoreductase A/GGG subunit precursor homolog mRNA, nuclear gene
3826	8633	13638	2.28	1.0E-42	7692027	NT	encoding mitochondrial protein, complete cds
3705	8709	13712	0.92	1.0E-42	5031610	NT	Homo sapiens rec (LOC51201), mRNA
3825	8827	13834	1.08	1.0E-42	AL163287.2	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
4124	9119	14105	1.89	1.0E-42	AL163280.2	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
4462	9452	14433	0.75	1.0E-42	AW819617.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C067
4602	9590	14577	2.94	1.0E-42	5803122	NT	Homo sapiens chromosome 21 segment HS21C080
4602	9590	14578	2.94	1.0E-42	5803122	NT	RC3-ST0197-161099-012-a03 ST0197 Homo sapiens cDNA
4634	9619	14811	5.84	1.0E-42	4506758	NT	Homo sapiens proteasome inhibitor (Pi31), mRNA
644	5672	10676	12.63	8.0E-43	AV736824.1	EST_HUMAN	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
644	5672	10677	12.63	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
691	5715	10729	5.28	8.0E-43	8923276	NT	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
691	5715	10730	5.28	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
691	5715	10731	5.28	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
3556	8563	13569	8.21	7.0E-43	AW246442.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
1324	6322		24.66	8.0E-43	AA491890.1	EST_HUMAN	2822281.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822281 5'
2516	7484		2.86	6.0E-43	AV708201.1	EST_HUMAN	ne72d08.s1 NCL CGAP_Ew1 Homo sapiens cDNA clone IMAGE:909803 similar to gb:U05095 60S RIBOSOMAL PROTEIN L30 (HUMAN);
							AV708201 ADC Homo sapiens cDNA clone ADCACC10 5'

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
142	5208		1.96	5.0E-43	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
489	5535	10541	3.04	5.0E-43	AA382780.1	EST_HUMAN	EST96033 Testis 1 Homo sapiens cDNA 5' end
2773	7794	12814	1.62	5.0E-43	AV732578.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTFANC06 5'
898	7698	11007	5.71	4.0E-43	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1194	6195		3.19	3.0E-43	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1656	6652	11724	4.45	3.0E-43	X97869.1	NT	H. sapiens gene encoding La autoantigen
3491	8499	13513	1.29	3.0E-43	S69002.1	NT	AML1-EVI-1=AML1-EVI-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA Mutant, 6938 nt]
4187	9182	14148	0.69	3.0E-43	AA548154.1	EST_HUMAN	nk55408.st NCI_CGAP_P7 Homo sapiens cDNA clone IMAGE:1017419
183	5246		21.1	2.0E-43	AI190764.1	EST_HUMAN	q61c09.x1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:1733968 3' similar to contains PTR7.3
1610	6606	11669	2.07	1.0E-43	AF154836.1	NT	PTR7 PTR7 repetitive element;
1610	6608	11670	2.07	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1686	6682	11737	1.71	1.0E-43	AL163284.2	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
2652	7612	12722	4.87	1.0E-43	BF348283.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
879	5897	10938	4.62	8.0E-44	AI222985.1	EST_HUMAN	602022313F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157666 5'
879	5897	10939	4.62	8.0E-44	AI222985.1	EST_HUMAN	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
4721	9706	14692	1.2	8.0E-44	AW373185.1	EST_HUMAN	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
4721	9706	14693	1.2	8.0E-44	AW373185.1	EST_HUMAN	RC5-BT0503-081299-011-g12 BT0503 Homo sapiens cDNA
651	5879		1.08	7.0E-44	RO6035.1	EST_HUMAN	RC5-BT0503-081299-011-g12 BT0503 Homo sapiens cDNA
2172	7151	12270	1.31	7.0E-44	5031886	NT	ye89e01.r1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:124920 5'
2896	7915	12835	2.47	7.0E-44	AF048729.1	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
2896	7915	12835	2.47	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3772	8775	13778	2.74	7.0E-44	AL163284.2	NT	Homo sapiens minisatellite ms32 repeat region
4119	9113	14098	1.21	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 segment HS21C084
4118	9113	14099	1.21	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
301	5358		3.07	5.0E-44	AJ289890.1	NT	Homo sapiens chromosome 21 unknown mRNA
330	5382		1.86	5.0E-44	AJ289890.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
3330	8340	13358	3.09	4.0E-44	AL163303.2	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
4854	9835		1.24	4.0E-44	AI452225.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
1748	6742		1.97	3.0E-44	6912477	NT	tt11d02.x1 NCI_CGAP_Pen1 Homo sapiens cDNA clone IMAGE:2130147 3'
2460	7429	12546	1.98	3.0E-44	BE880626.1	EST_HUMAN	Homo sapiens karyopherin alpha 6 (importin alpha7) (KPNAB6), mRNA

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3024	8041	13050	6.08	3.0E-44	AA169851.1	EST_HUMAN	zp18b05.r1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609777 5'
1032	6042	11071	2.58	2.0E-44	4826685	NT	Homo sapiens DEAD/1 (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1032	6042	11071	2.58	2.0E-44	4826685	NT	Homo sapiens DEAD/1 (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1188	6189	11226	4.87	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1188	6189	11227	4.87	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1283	6281	11337	4.09	2.0E-44	AF133588.1	NT	Homo sapiens RAB36 (RAB36) mRNA, complete cds
1351	8348	11398	1.58	2.0E-44	BE486325.1	EST_HUMAN	hwr14g06.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182838 3' similar to SW:OXYB_HUMAN
2081	7072	12186	2.43	2.0E-44	AF070651.1	NT	P22059 OXYSTEROL-BINDING PROTEIN. ;
2536	7501		3.54	2.0E-44	5901933	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
3390	8398	13424	1.97	2.0E-44	D87675.1	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (GLAPS4), mRNA
4437	9427	14411	1.85	2.0E-44	AW864379.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
4644	9629	14623	1.01	2.0E-44	7706128	NT	PMA-SN0016-120500-003-a04 SN0016 Homo sapiens cDNA
4644	9629	14624	1.01	2.0E-44	7706128	NT	Homo sapiens oxysterol 7alpha-hydroxylase (CYP39A1), mRNA
53	5134	10130	8.52	1.0E-44	7657334	NT	Homo sapiens oxysterol 7alpha-hydroxylase (CYP39A1), mRNA
53	5134	10131	8.52	1.0E-44	7657334	NT	Homo sapiens oxysterol 7alpha-hydroxylase (CYP39A1), mRNA
575	5607	10606	1.72	1.0E-44	AW863132.1	EST_HUMAN	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA
1178	6180		1.29	1.0E-44	AW994803.1	EST_HUMAN	RC1-CT0249-030300-026-R12 CT0249 Homo sapiens cDNA
1539	6537		3.86	1.0E-44	AL163303.2	NT	RC1-BN0039-110300-012-B01 BN0039 Homo sapiens cDNA
2163	7142	12259	3.27	1.0E-44	AA434554.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
2163	7142	12260	3.27	1.0E-44	AA434554.1	EST_HUMAN	zw53d02.r1 Soares_t01a_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR13 THR repetitive element ;
2685	7643	12758	1.26	1.0E-44	AF189779.1	NT	contains THR13 THR repetitive element ;
3642	8648		4.21	1.0E-44	AA455869.1	EST_HUMAN	Homo sapiens transcription factor IGDM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, complete cds; and L-type calcium channel a2
4945	9922	14900	0.76	1.0E-44	AJ130755.1	NT	aa01c09.s1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:811884 3'
4945	9922	14901	0.76	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
4445	9435	14418	1.61	9.0E-45	8922391	NT	Homo sapiens alpha satellite DNA, M1 monomer type
4445	9435	14419	1.61	9.0E-45	8922391	NT	Homo sapiens hypodermal protein FLJ10379 (FLJ10379), mRNA
2453	7423	12538	4.1	8.0E-45	5174718	NT	Homo sapiens hypodermal protein FLJ10379 (FLJ10379), mRNA
4810	9889	14862	8.47	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
2887	7906		1.91	7.0E-45	AL160131.1	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
							Novel human gene mapping to chromosome 22

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1521	6518		1.01	6.0E-45	A1675425.1	EST_HUMAN	wb99cd6.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2313802 3' similar to contains L1.11 L1 repetitive element;
3871	8872		9.19	6.0E-45	AW157570.1	EST_HUMAN	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782809 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A;
881	5899		1.17	5.0E-45	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1956	6942	12044	2.41	5.0E-45	BF333627.1	EST_HUMAN	CM4-CN0044-180200-515-101 CN0044 Homo sapiens cDNA
3137	8153	13176	2.09	5.0E-45	A1523786.1	EST_HUMAN	lg94f07.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE
1126	6131	11161	13.11	4.0E-45	X95826.1	NT	H.sapiens ART4 gene
2229	7206	12321	3.69	4.0E-45	BE265622.1	EST_HUMAN	601194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5'
3946	8944	13934	1.07	4.0E-45	4503422	NT	Homo sapiens dUTP pyrophosphatase (DUT) mRNA
3256	8269		1.58	3.0E-45	T71480.1	EST_HUMAN	yd35f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
3971	8269		1.78	3.0E-45	T71480.1	EST_HUMAN	yd35f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
2429	7400		1.54	2.0E-45	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
2862	7980	12994	1.28	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
124	5443		3.37	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608183 5'
406	5443		3.74	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608183 5'
469	5505	10519	1.3	1.0E-45	4508412	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
1155	6159	11193	1.76	1.0E-45	7657290	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3030	8047	13057	7.83	1.0E-45	U32166.1	NT	Human pro-a2 chain of collagen type XI (COL11A2) gene, complete cds
3412	8421	13450	0.79	1.0E-45	8659558	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
4350	8341	14322	4.49	1.0E-45	BE396633.1	EST_HUMAN	601289116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619803 5'
2374	7346	12466	26.07	8.0E-46	A1433261.1	EST_HUMAN	h32f08.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_ma2
2374	7346	12467	26.07	8.0E-46	A1433261.1	EST_HUMAN	h32f08.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_ma2
2177	7156	12276	1.08	7.0E-46	U46007.1	NT	Rattus norvegicus espin mRNA, complete cds
4447	9437		9.38	7.0E-46	BE386165.1	EST_HUMAN	601277292F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
4682	9647		1.73	7.0E-46	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
2881	7639	12754	3.59	6.0E-46	A1894381.1	EST_HUMAN	wm31108.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
2881	7639	12755	3.59	6.0E-46	A1894381.1	EST_HUMAN	wm31108.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
204	5268		4.44	5.0E-46	AL163210.2	NT	MER19 repetitive element;
							Homo sapiens chromosome 21 segment HS21C010

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3450	8458	13484	1.07	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupskl_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
3450	8458	13485	1.07	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupskl_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
635	5663		2.5	4.0E-46	AA601143.1	EST_HUMAN	nd54e09.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_rna1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1665	6661	11735	8.01	4.0E-46	AW770544.1	EST_HUMAN	hi86c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_rna1 LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element ;
1665	6661	11736	8.01	4.0E-46	AW770544.1	EST_HUMAN	hi86c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_rna1 LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element ;
2668	7625	12737	2.58	4.0E-46	M18048.1	NT	Human endogenous retrovirus RTVL-H2
4263	9285	14272	0.97	4.0E-46	AB014522.1	NT	Homo sapiens mRNA for KIAA0622 protein, partial cds
4263	9285	14273	0.97	4.0E-46	AB014522.1	NT	Homo sapiens mRNA for KIAA0622 protein, partial cds
2222	7199	12319	1.23	3.0E-46	7657203	NT	Homo sapiens acidic 82 kDa protein mRNA (HSU15532), mRNA
2361	7335	12452	2.18	3.0E-46	AF160212.1	NT	Homo sapiens VAMP-associated 33 kDa protein mRNA, complete cds
4269	9262	14252	0.72	3.0E-46	4506376	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4630	9815	14605	1.22	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda
4630	9815	14606	1.22	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda
827	5847	10884	8.39	2.0E-46	AA468846.1	EST_HUMAN	ne08a09.s1 NCL_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element ;
1601	6597	11659	2.53	2.0E-46	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
4815	9799	14780	1.31	2.0E-46	AA399286.1	EST_HUMAN	z159e02.r1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:726650 5' similar to SW:RSP1_MOUSE Q01730 RSP-1 PROTEIN ;
1213	6212	11252	5.7	1.0E-46	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
1538	6536	11594	1.27	1.0E-46	7662177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
1538	6536	11595	1.27	1.0E-46	7662177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2218	7195	12317	3.91	1.0E-46	AW978516.1	EST_HUMAN	EST390625 MAGP resequences, MAGP Homo sapiens cDNA
2336	7310	12431	2.62	1.0E-46	H97330.1	EST_HUMAN	EST485095 WATM1 Homo sapiens cDNA clone 485095
3176	8192	13213	8.47	1.0E-46	AA631912.1	EST_HUMAN	np78b02.s1 NCL_CGAP_P2 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:X76717 H.sapiens MT-1 mRNA, (HUMAN);
4723	9708		3	1.0E-46	AB023197.1	NT	Homo sapiens mRNA for KIAA0980 protein, partial cds

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
757	5778		3.81	9.0E-47	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4776	9760	14747	2.41	9.0E-47	AW770928.1	EST_HUMAN	h193e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009534 3' similar to TR:O75703 O75703
1772	8784	11852	90.6	8.0E-47	Y18536.1	NT	HYPOTHETICAL 12.4 KD PROTEIN.
1772	8784	11853	80.6	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
2844	7604	12717	1.38	8.0E-47		NT	Homo sapiens HLA-C gene, exon 5, individual 19323
2957	7976	12991	1.73	8.0E-47	5453956	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
2477	7446	12559	1.23	6.0E-47	AJ228043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
1378	6373	11423	5.93	4.0E-47	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
540	5575	10580	3.84	3.0E-47	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
540	5575	10581	3.84	3.0E-47	BE907634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
808	5829	10860	4.98	3.0E-47	BE907634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
931	5948	10982	7.81	3.0E-47	N57483.1	EST_HUMAN	Y64b04.s1 Soares_multiple_sclerosis_2NblMSP Homo sapiens cDNA clone IMAGE:277327 3'
3230	8245	13267	0.94	3.0E-47	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C008
3659	8861		6.7	3.0E-47	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4237	9231	14214	1.25	3.0E-47	U93181.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
147	5213	10227	1.29	2.0E-47	M12859.1	NT	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
953	5869	11001	2.67	2.0E-47	4505318	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
953	5869	11002	2.67	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C005
1558	6555	11616	2	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C008
1638	6635	11705	3.76	2.0E-47	7662109	NT	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
4221	9215	14184	1.6	2.0E-47	AA524514.1	EST_HUMAN	ng43h12.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:937607 3'
4259	9253	14240	1.82	2.0E-47	4504866	NT	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4378	9263	14241	1.82	2.0E-47	AA569592.1	EST_HUMAN	nf23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
4378	9367	14347	2.23	2.0E-47	AA569592.1	EST_HUMAN	nf23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
4687	9652	14640	1.32	2.0E-47	5174648	NT	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA
1381	6378	11426	4.13	2.0E-47	AW985166.1	EST_HUMAN	EST377239 IMAGE resequences, MAGI Homo sapiens cDNA
3731	8735	13732	2.17	1.0E-47	AJ333429.1	EST_HUMAN	qp99h03.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1931189 3'
3731	8735	13733	2.17	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
4904	8883	14854	3.23	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
1575	6572	11633	3.85	9.0E-48	AF223391.1	NT	RC3-ST0197-130400-017-h02 ST0197 Homo sapiens cDNA
1231	8230		1.49	8.0E-48	4501900	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
							Homo sapiens aminocyclase 1 (ACY1), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1232	6230		1.54	8.0E-48	4501900	NT	Homo sapiens aminocyclase 1 (ACY1), mRNA
3062	8079	13092	3.91	8.0E-48	AW768477.1	EST_HUMAN	h161b03.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
3062	8079	13093	3.91	8.0E-48	AW768477.1	EST_HUMAN	h161b03.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
487	5524		1.31	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
488	5524		19.03	7.0E-48	AB033035.1	NT	Homo sapiens tousel-like kinase 1 (TLK1), mRNA
1467	6464	11523	1.05	7.0E-48	6912719	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1597	6593	11654	6.73	7.0E-48	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
3518	8528	13537	7.89	6.0E-48	AI761111.1	EST_HUMAN	w69h03.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398813 3'
3237	10046	13272	1.51	5.0E-48	4828891	NT	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
1831	6917	12015	28.02	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
1831	6917	12016	28.02	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
4125	8120		0.89	3.0E-48	AA009541.1	EST_HUMAN	z04g03.r1 Soares fetal liver spleen INFLS S1 Homo sapiens cDNA clone IMAGE:428844 5'
5	5088	10071	1.14	2.0E-48	AA465007.1	EST_HUMAN	z60c03.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:810052 5'
48	5127	10118	2.18	2.0E-48	AA631940.1	EST_HUMAN	fmc7 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR17-26
4401	8392	14376	0.95	2.0E-48	BE246065.1	EST_HUMAN	TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project TCBA Homo sapiens cDNA clone TCBAP3842
4803	9787	14769	1.1	2.0E-48	T03176.1	EST_HUMAN	FB2E2 Fetal brain, Stragene Homo sapiens cDNA clone FB2E2 3'end
4803	9787	14770	1.1	2.0E-48	T03176.1	EST_HUMAN	FB2E2 Fetal brain, Stragene Homo sapiens cDNA clone FB2E2 3'end
5084	10033	15000	1.11	2.0E-48	AW470877.1	EST_HUMAN	xm67a10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2689242 3'
57	5137	10135	8.01	1.0E-48	7706534	NT	Homo sapiens dispiatin resistance-associated overexpressed protein (LOC51747), mRNA
862	5881	10922	4.37	1.0E-48	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1059	6088	11098	3.2	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1059	6088	11099	3.2	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1277	6276	11317	4.07	1.0E-48	5032032	NT	Homo sapiens RNA binding motif protein 6 (RBM6) mRNA
1874	6863	11952	15.16	1.0E-48	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3408	8417	13445	1.25	1.0E-48	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
4959	8936	14914	0.91	1.0E-48	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1959	6945	12047	0.92	8.0E-49	AB026497.1	NT	Mus musculus MyoPDZ mRNA for myosin containing PDZ domain, complete cds
139	5430	10445	4.24	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
139	5430	10446	4.24	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
392	5430	10445	3.24	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
392	5430	10446	3.24	7.0E-49	5729980	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
393	5430	10445	2.99	7.0E-49	5729980	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
393	5430	10446	2.89	7.0E-49	5729980	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
1201	6202	11239	3.59	7.0E-49	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
197	5261	10274	180.31	6.0E-49	AW731740.1	EST_HUMAN	ba59g05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800504.3' similar to gb:X17206.40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
1340	6338	11387	0.99	6.0E-49	BF038269.1	EST_HUMAN	601457738F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3861272 5'
1340	6338	11388	0.89	6.0E-49	BF038269.1	EST_HUMAN	601457738F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3861272 5'
3999	8995	13983	0.98	6.0E-49	AL162091.1	EST_HUMAN	DKFZp761A138_s1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A138 3'
702	5726	10741	7.25	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
702	5726	10742	7.25	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1758	6751	11835	3.85	6.0E-49	AA172121.1	EST_HUMAN	zp29c07.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610860 5' similar to TR:G233226 G233226 RTVL-H PROTEIN; contains LTR7.13 LTR7 LTR7 repetitive element;
2677	7635	12750	7.57	5.0E-49	U17714.1	NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds
3199	8215	13236	9.74	5.0E-49	11436355	NT	Homo sapiens similar to ribosomal protein S27 (melalopastimulin 1) (H. sapiens) (LOC63362), mRNA X08801.x1 NCJ_CGAP_U14 Homo sapiens cDNA clone IMAGE:2675593 3' similar to WP:B0350.2B CE06703;
521	5556	10558	22.86	4.0E-49	AW189533.1	EST_HUMAN	H. sapiens mRNA for acetyl-CoA carboxylase
558	5590	10591	0.9	3.0E-49	X88988.1	NT	ze31c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1 repetitive element;
2575	7538		1.21	3.0E-49	AA016131.1	EST_HUMAN	Human type IV collagen (COL4A6) gene, exon 40
4824	8808	14790	2.5	3.0E-49	U48999.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4999	8970		0.94	3.0E-49	L78810.1	NT	MIR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
653	5881		3.08	2.0E-49	BE165980.1	EST_HUMAN	y23d06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:282571 5'
3151	8167	13187	1.44	2.0E-49	N28448.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
888	5906		6.68	1.0E-49	BF036327.1	EST_HUMAN	Homo sapiens keratin 18 (KRT18) mRNA
1522	6519	11575	27.09	1.0E-49	4557887	NT	601115769F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3358273 5'
1765	6757	11843	5.52	1.0E-49	BE255216.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C002
169	5234	10244	2.76	8.0E-50	AL163202.2	NT	Homo sapiens mRNA for VIP receptor 2
709	5733	10749	1.82	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
709	5733	10750	1.82	8.0E-50	X95097.2	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
1726	6721	11789	13.5	8.0E-50	4501890	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2411	7382	12500	1.29	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51874), mRNA
2411	7382	12501	1.29	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51874), mRNA
2827	7597	12699	3.51	8.0E-50	4826658	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA
4217	9210		0.88	6.0E-50	BE784381.1	EST_HUMAN	601589565F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3943577 5'
1757	6750	11833	1.19	5.0E-50	BF332938.1	EST_HUMAN	CMO-BT0792-300500-398-505 BT0792 Homo sapiens cDNA
1757	6750	11834	1.19	5.0E-50	BF332938.1	EST_HUMAN	CMO-BT0792-300500-398-505 BT0792 Homo sapiens cDNA
906	5923		1.83	4.0E-50	AA601143.1	EST_HUMAN	nc54e09.s1 NCI CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_ma1
3365	8373	13393	0.98	4.0E-50	AL163248.2	NT	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1898	6886		2.31	3.0E-50	M18048.1	NT	Homo sapiens chromosome 21 segment HS21C048
2447	7417	12532	1.05	3.0E-50	BE259186.1	EST_HUMAN	Human endogenous retrovirus RTVL-H2
3225	8240	13262	0.89	3.0E-50	AA746142.1	EST_HUMAN	601109717F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350309 5'
							6003106.s1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322827 3'
5032	10003	14974	1.04	3.0E-50	AW593866.1	EST_HUMAN	hg26e01.x1 NCI CGAP_GC6 Homo sapiens cDNA clone IMAGE:2946744 3' similar to SW:C1TC_HUMAN
769	5780		14.02	2.0E-50	AF055066.1	NT	P11586 C-1-TETRAHYDROFOLATE SYNTHASE; CYTOPLASMIC ;contains Alu repetitive element;
1063	6071	11103	6.6	2.0E-50	4557752	NT	Homo sapiens MHC class 1 region
1417	6414	11475	1.28	2.0E-50	AF138303.1	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3214	8228	13250	0.78	2.0E-50	AF111168.2	NT	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
4138	9133	14116	1.11	2.0E-50	D86424.1	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
459	5498	10507	1.74	1.0E-50	AL163209.2	NT	Mus musculus mRNA for high-sulfur keratin protein; partial cds
2304	7278		7.62	1.0E-50	AJ271735.1	NT	Homo sapiens chromosome 21 segment HS21C009
							Homo sapiens Xq pseudautosomal region; segment 1/2
4435	9425	14410	12.15	8.0E-51	AA610842.1	EST_HUMAN	np89e08.s1 NCI CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:X12671_ma1
							HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
2950	7669	12986	1.33	7.0E-51	AW274720.1	EST_HUMAN	Q9Z340.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q9Z340
3209	8224	13246	1.63	7.0E-51	AW889219.1	EST_HUMAN	QV4-NT0028-200400-180-d05 NT0028 Homo sapiens cDNA
							Q9Z340.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q9Z340
3282	8294	13319	0.82	7.0E-51	AW274720.1	EST_HUMAN	Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
4043	9039	14029	1.25	7.0E-51	AL079628.1	EST_HUMAN	DKFZp434B2229 r1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434B2229 5'
4043	9039	14030	1.25	7.0E-51	AL079628.1	EST_HUMAN	DKFZp434B2229 r1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434B2229 5'
4225	9219	14198	2.54	7.0E-51	AW295603.1	EST_HUMAN	UJ-H-BW0-elp-b-05-0-UJ.s1 NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729817 3'
1498	6484	11549	1.18	6.0E-51	6678763	NT	Homo sapiens putative DNA binding protein (M98), mRNA

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1934	6920	12019	3.34	6.0E-51	7657268	NT	Homo sapiens KIAA0929 protein Mix2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
3393	8401	13427	15.79	6.0E-51	7657266	NT	Homo sapiens KIAA0929 protein Mix2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
763	5804	10834	5.88	5.0E-51	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
794	5815	10848	1.74	6.0E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
976	7738	11024	1.07	6.0E-51	AL133204.1	NT	Novel human gene mapping to chromosome X
1571	6566	11630	1.42	5.0E-51	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
2517	7495	12601	6.01	5.0E-51	AJ007568.1	NT	Homo sapiens mRNA for nucleoporin 155
3841	8843	13850	3.67	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
3841	8843	13851	3.67	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4900	9879	14848	1.64	5.0E-51	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
135	5201	10217	20.61	3.0E-51	AI587348.1	EST_HUMAN	trf1c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1157	6161	11195	35.84	3.0E-51	AI587348.1	EST_HUMAN	trf1c08.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1882	6871	11860	1.08	3.0E-51	AA211296.1	EST_HUMAN	zq87g01.s1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:649008 3'
4200	9193	14175	2.01	3.0E-51	AL159142.1	NT	Novel human gene mapping to chromosome 22
385	5414	10427	2.45	2.0E-51	4507788	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
679	5704	10712	1.65	2.0E-51	BE391063.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
679	5704	10713	1.65	2.0E-51	BE391063.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
1849	6645	11718	6.38	2.0E-51	AA233352.1	EST_HUMAN	z30a06.r1 Stralagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:664880 5' similar to TR-G233226 G233226 RTVL-H PROTEIN; contains LTR7.13 LTR7 repetitive element;
3848	8854	13860	2.94	2.0E-51	AI492415.1	EST_HUMAN	trf27g03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131732 3'
114	5186	10195	45.03	1.0E-51	4503528	NT	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
1462	6469		51.24	1.0E-51	AV742248.1	EST_HUMAN	AV742248 CB Homo sapiens cDNA clone CBFBCC12 5'
151	5217	10230	7.75	8.0E-52	AA720574.1	EST_HUMAN	hw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element;
1488	6483	11522	1.35	8.0E-52	XB4900.1	NT	H. sapiens mRNA for laminin-5, alpha3b chain
1614	6610	11674	2.31	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1614	6610	11675	2.31	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3888	6610	11674	6.2	8.0E-52	11668028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
3888	6610	11675	6.2	8.0E-52	11668028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1655	6651	11723	3.39	6.0E-52	AF109807.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4318	9310	14296	2.8	5.0E-52	Z76898.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA18H7
1622	6619	11685	1.32	4.0E-52	AF257318.1	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
1750	6744	11823	2.08	4.0E-52	4758843	NT	Homo sapiens nucleoporin 158kD (NUP155) mRNA
3826	8828	13835	0.81	4.0E-52	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4514	9504	14484	1.26	4.0E-52	5174590	NT	Homo sapiens 5,10-methylene-tetrahydrofolate dehydrogenase, 5,10-methylene-tetrahydrofolate cyclohydrolase, 10-formyltetrahydrofolate synthetase (MTHFD) mRNA
3975	8973	10592	10.25	3.0E-52	11437042	NT	Homo sapiens hypothetical protein FLJ10675 (FLJ10675), mRNA
558	5592	10592	1.85	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete (retroviral segment)
558	5592	10593	1.85	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete (retroviral segment)
1718	6713	11790	1.15	2.0E-52	AB007899.1	NT	Homo sapiens KIAA0439 mRNA, partial cds
1964	6949	12052	1	2.0E-52	AB033075.1	NT	Homo sapiens mRNA for KIAA1249 protein, partial cds
2426	7397	12518	3.12	2.0E-52	BE207575.1	EST_HUMAN	bb56b07.y1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:X18493 M.musculus mRNA for Zpf-1 zinc finger protein (MOUSE);
2862	7621		19.48	2.0E-52	BF677892.1	EST_HUMAN	602084710F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5'
4818	9802	14782	3.17	2.0E-52	AL137189.3	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
4853	9834	14808	1.1	2.0E-52	AI141802.1	EST_HUMAN	qa56a05.s1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
4853	9834	14809	1.1	2.0E-52	AI141802.1	EST_HUMAN	qa56a05.s1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
529	5564	10568	1.37	1.0E-52	AA634445.1	EST_HUMAN	zu75h12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743879 3'
1354	6351	11401	9.59	1.0E-52	4504026	NT	Homo sapiens glutamate-aminoligase (glutamine synthase) (GLUL) mRNA
2465	7434		1.67	1.0E-52	4502238	NT	Homo sapiens arylsulfolase D (ARSD), transcript variant 1, mRNA
2885	8003	13015	1.89	1.0E-52	S61070.1	NT	pol=reverse transcriptase homolog (retroviral element) [human, endogenous retroviral element RTVL-Hp1, Genomic, 660 nt]
3702	8708	13708	1.3	9.0E-53	4506084	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
4267	9260	14250	1.22	9.0E-53	AF001446.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 3
5033	10004	14976	1.19	9.0E-53	AB040937.1	NT	Homo sapiens mRNA for KIAA1504 protein, partial cds
3882	8880	13965	15.99	6.0E-53	4758543	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
50	5131	10125	1.53	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
50	5131	10126	1.53	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085

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4675	9660	14643	0.98	4.0E-53	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
2589	7552	12667	1.47	3.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3647	8653	13659	1.94	3.0E-53	AW050836.1	EST_HUMAN	wz22c07.x1 Soares_Dieckgraeft_colon_NHCD Homo sapiens cDNA clone IMAGE:2558796 3'
4457	8447	14427	0.73	3.0E-53	AW803563.1	EST_HUMAN	IL2-UM0081-240300-055-D03 UM0081 Homo sapiens cDNA
455	5492		3.58	2.0E-53	AA366556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
2266	7243	12360	20.13	2.0E-53	U78027.1	NT	(L44L) and FTP3 (FTP3) genes, complete cds
2466	7435		7.48	2.0E-53	4502316	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP6E), mRNA
3147	8163	13183	0.92	2.0E-53	7705687	NT	Homo sapiens leucine aminopeptidase (LOC51056), mRNA
3172	8188	13210	2.53	2.0E-53	AF083822.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 6
3947	8945	13935	2.5	2.0E-53	M61873.1	NT	Human Knueppel-related DNA-binding protein (TF34) gene, partial cds
4365	9356	14336	0.92	2.0E-53	4506962	NT	Homo sapiens SKAP55 homologue (SKAP-HOM) mRNA
1420	8417	11477	1.56	1.0E-53	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
3325	8335	13355	1.23	1.0E-53	AB026698.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4807	9791	14773	1.54	1.0E-53	BE286386.1	EST_HUMAN	601176726F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531919 5'
5039	10010	14979	0.97	1.0E-53	AW967429.1	EST_HUMAN	EST368619 MAGI resequences, MAGI Homo sapiens cDNA
207	5271	10283	4.09	8.0E-54	BE386785.1	EST_HUMAN	601272863F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614031 5'
1799	8790	11880	2.71	8.0E-54	4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
4596	9584	14573	0.71	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
4598	9584	14574	0.71	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
383	5458	10475	1.58	7.0E-54	AA812537.1	EST_HUMAN	al78c12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1377046 3' similar to contains MER30.13 MER30 repetitive element;
1794	8785	11875	1.37	7.0E-54	Y16645.1	NT	Homo sapiens mRNA for monocyte chemotactic protein-2
2142	7121	12237	4.24	7.0E-54	N27177.1	EST_HUMAN	yw68d12.s1 Soares_placenta_8to9weeks_2NbHP8t59W Homo sapiens cDNA clone IMAGE:257399 3' similar to contains LTR7 b3 LTR7 repetitive element;
5043	10014	14883	1.08	7.0E-54	A1276760.1	EST_HUMAN	q164e10.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1677130 3'
23	5103	10088	5.96	6.0E-54	AB003618.1	NT	Homo sapiens DNA for MICB, exon 4, 5 and partial cds
384	5459	10476	1.73	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
384	5459	10477	1.73	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3210	8225	13247	2.1	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3898	8898	13898	1.11	6.0E-54	4502872	NT	Homo sapiens chloride channel 6 (CLCN6) mRNA

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4696	9681	14864	1.19	6.0E-54	4505808	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4724	9709		2.36	6.0E-54	Y09846.1	NT	H. sapiens shc pseudogene, p68 isoform
4841	9709		2.18	6.0E-54	Y09846.1	NT	H. sapiens shc pseudogene, p68 isoform
2090	7071	12185	3.25	5.0E-54	P51523	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
182	5245		263.62	4.0E-54	AF110103.1	NT	Tupala belangeri beta-actin mRNA, partial cds
941	5958	10991	140.55	4.0E-54	AA308764.1	EST_HUMAN	EST177698 Jurkat T-cells V1 Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
1769	6781	11848	2.55	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1769	6781	11849	2.55	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3131	8147		1.39	4.0E-54	A1935086.1	EST_HUMAN	w26d11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329269 3' similar to TR:002711
92	5169	10179	30.76	3.0E-54	AA313487.1	EST_HUMAN	002711 PRO-POL-DUTPASE POLYPROTEIN ;
2551	7516		1.04	3.0E-54	A1908757.1	EST_HUMAN	EST185371 Colon carcinoma (HCC) cell line Homo sapiens cDNA
636	5664	10688	6.13	2.0E-54	5031900	NT	IL-BT189-190389-007 BT189 Homo sapiens cDNA
1347	6344	11395	2.11	2.0E-54	4507164	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
1515	6513	11569	1.19	2.0E-54	AA655008.1	EST_HUMAN	n178a09.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1204600 similar to contains element L1 repetitive element ;
2469	7437	12554	1.47	2.0E-54	AW163175.1	EST_HUMAN	au92g03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5' similar to SW:CU11_HUMAN Q13616 CULLIN HOMOLOG 1 ;
2524	7490	12610	1.65	2.0E-54	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2824	7845	12865	1.51	2.0E-54	AW057524.1	EST_HUMAN	wy60b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552927 3' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;
3472	8480		7.32	2.0E-54	AA532925.1	EST_HUMAN	n145g09.s1 NCI_CGAP_Pr9 Homo sapiens cDNA clone IMAGE:995488 similar to gb:X53777 60S RIBOSOMAL PROTEIN L23 (HUMAN);
4082	8078		3.11	2.0E-54	4502642	NT	Homo sapiens chaperonin containing T-complex subunit 6 (CCT6) mRNA
4319	9311		1.14	2.0E-54	AF208161.1	NT	Homo sapiens syncytin precursor, mRNA, complete cds
5052	10023	14992	0.92	2.0E-54	4506982	NT	Homo sapiens SKAP55 homologue (SKAP-HOM) mRNA
4341	9332		1.35	1.0E-54	BF315418.1	EST_HUMAN	601889230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5'
1298	6296		1.8	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1065	6073	11108	1.85	7.0E-55	R09346.1	EST_HUMAN	y26e04.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127988 5' similar to SP:C561_BOVIN P10897 CYTOCHROME ;
1733	6728	11804	2.5	5.0E-55	AA704971.1	EST_HUMAN	z195b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
1733	6728	11805	2.5	5.0E-55	AA704971.1	EST_HUMAN	z195b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
4628	9811	14600	1.31	5.0E-55	AW206021.1	EST_HUMAN	UJ-H-B11-efy-g-09-0-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723536 3'

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56	7712	10134	6.49	4.0E-55	AW957994.1	EST_HUMAN	EST370064 MAGE resequences, MAGE Homo sapiens cDNA
684	6580	10699	29.4	4.0E-55	4829973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1414	6412	11471	1.58	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3789), mRNA
1414	6412	11472	1.58	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3789), mRNA
1483	6480		1.43	4.0E-55	BF061411.1	EST_HUMAN	752b10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3390043 3' similar to contains L1.13 L1 repetitive element:
1974	6959	12084	1.95	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
1974	6959	12085	1.95	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2032	7015	12123	3.3	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90KD) (DGKG) mRNA
2032	7015	12124	3.3	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90KD) (DGKG) mRNA
2247	7224	12344	4.51	4.0E-55	4507794	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
3206	8221	13243	1.2	4.0E-55	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4985	9959	14936	2.08	4.0E-55	BE698671.1	EST_HUMAN	RC2-UT0023-290700-011-f03 UT0023 Homo sapiens cDNA
378	5423	10438	2	2.0E-55	X67147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
547	6581		1.08	2.0E-55	M10976.1	NT	Human endogenous retrovirus DNA (4-1), complete retroviral segment
641	5669	10673	4.78	2.0E-55	4507296	NT	Homo sapiens syntaxin-binding protein 1 (STXB1) mRNA, and translated products
2889	7608	12928	1.7	2.0E-55	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
4829	8614	14604	2.97	2.0E-55	BE719986.1	EST_HUMAN	CM1-HT0878-150800-357-g03 HT0878 Homo sapiens cDNA
95	5172	10182	2.86	1.0E-55	4505060	NT	Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA
189	5253	10264	113.02	1.0E-55	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds
599	5602	10600	14.24	1.0E-55	AJ026718.1	EST_HUMAN	ov85g09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1844160 3'
1132	6137	11168	6.88	1.0E-55	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1911	6897	11991	5	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867027 5'
1911	6897	11992	5	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867027 5'
2263	7240		6.39	1.0E-55	5803174	NT	Homo sapiens SMA3 (SMA3), mRNA
2446	7416	12531	63.73	1.0E-55	X13111.1	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2483	7451	12584	3.08	1.0E-55	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2483	7451	12585	3.08	1.0E-55	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2538	7503	12622	14.65	1.0E-55	LS4057.1	NT	Homo sapiens CLP mRNA, partial cds
2717	7674	12787	0.98	1.0E-55	AB033045.1	NT	Homo sapiens mRNA for KIAA1219 protein, partial cds
3389	8397	13422	1.83	1.0E-55	5174590	NT	Homo sapiens 5,10-methylenetetrahydrofolate dehydrogenase, 5,10-methylenetetrahydrofolate cyclohydrolase, 10-formyltetrahydrofolate synthetase (MTHFD) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3389	8397	13423	1.83	1.0E-55	5174590	NT	Homo sapiens 5,10-methylenetetrahydrofolate dehydrogenase, 5,10-methylenetetrahydrofolate
3883	8884	13882	3.88	1.0E-55	AL163267.2	NT	cyclohydrolase, 10-formyltetrahydrofolate synthetase (MTHFD) mRNA
4170	9165	14152	1.64	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C037
4592	9580		1.01	1.0E-55	N77261.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
4958	8935	14913	1.08	1.0E-55	8923125	NT	w44g03.11 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:245620 5'
5015	8986	14962	2.2	1.0E-55	BE077198.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20126 (FLJ20126), mRNA
2659	7619	12730	3.83	7.0E-56	H19934.1	EST_HUMAN	RC5-BT0605-150200-031-B11 BT0605 Homo sapiens cDNA
1653	6849	11721	1.83	5.0E-56	AW99712.1	EST_HUMAN	RC3-BN0053-170200-011-101 BN0053 Homo sapiens cDNA
28	5108	10092	44.14	4.0E-56	AF141349.1	NT	THR repetitive element
28	5108	10093	44.14	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2636	7596	12709	7.3	4.0E-56	4507728	NT	Homo sapiens beta-tubulin mRNA, complete cds
2636	7596	12710	7.3	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2740	5557	10560	3.58	4.0E-56	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1322	6320	11368	3.78	3.0E-56	8924029	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
1727	6722	11800	3.22	3.0E-56	6912743	NT	Homo sapiens 5'-3' exoribonuclease 2 (XRN2), mRNA
2089	7070	12184	1.19	3.0E-56	6912697	NT	Homo sapiens oncogene TC21 (TC21), mRNA
3052	8069	13078	1.47	3.0E-56	AA325828.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3052	8069	13079	1.47	3.0E-56	AA325828.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3745	8749		2.03	3.0E-56	AF055066.1	NT	Homo sapiens MHC class 1 region
3818	8920	13827	1.28	3.0E-56	BE393512.1	EST_HUMAN	601310203F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631848 5'
4263	9256	14246	1.01	3.0E-56	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSGR1), mRNA
4300	9292	14279	4.75	3.0E-56	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. ceriseiae homolog)-like (SKIV2L), mRNA
4440	9430	14414	2.24	3.0E-56	6912693	NT	Homo sapiens phosphatidylinositol transfer protein, beta (PITPNB), mRNA
4941	9918	14898	0.72	3.0E-56	6912693	NT	Homo sapiens phosphatidylinositol transfer protein, beta (PITPNB), mRNA
4984	9918	14898	0.83	3.0E-56	6912593	NT	Homo sapiens phosphatidylinositol transfer protein, beta (PITPNB), mRNA
520	5555		1.87	2.0E-56	AA189818.1	EST_HUMAN	zq52a08.s1 Stralagens neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:845206 3'
723	7729	10765	1.67	2.0E-56	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-F10 BT0310 Homo sapiens cDNA
723	7729	10766	1.67	2.0E-56	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-F10 BT0310 Homo sapiens cDNA
2321	7296	12416	0.94	2.0E-56	M26061.1	NT	Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA, complete cds
2321	7296	12417	0.94	2.0E-56	M26061.1	NT	Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA, complete cds
2919	7838	12955	1.04	2.0E-56	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cde

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3242	8255		1.89	2.0E-56	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3458	8484	13491	1.29	2.0E-56	AV703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ADBCF-G10 5'
965	5980		4.42	1.0E-56	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
1489	6486	11541	2.19	1.0E-56	AA293038.1	EST_HUMAN	z154b09.1 Scores ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:726137 5' similar to gb:M94654
3590	8597	13601	2.28	1.0E-56	AW589833.1	EST_HUMAN	INTERLEUKIN ENHANCER-BINDING FACTOR (HUMAN);
3590	8597	13602	2.28	1.0E-56	AW589833.1	EST_HUMAN	hg23c11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2948452 3'
620	5647		1.82	9.0E-57	AW880885.1	EST_HUMAN	hg23c11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2946452 3'
4081	9075	14063	0.87	8.0E-57	4758279	NT	QV0-OT0033-070300-152-h03 OT0033 Homo sapiens cDNA
4081	9075	14064	0.87	9.0E-57	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
285	5352	10365	2.81	8.0E-57	AW816405.1	EST_HUMAN	Homo sapiens EphA4 (EPHA4) mRNA
873	5891	10932	7.02	8.0E-57	AW264599.1	EST_HUMAN	QV4-ST0234-181199-037-005 ST0234 Homo sapiens cDNA
1780	6772	11864	1.69	8.0E-57	AA498109.1	EST_HUMAN	xt05d10.x1 NCI_CGAP_Bms3 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gb:U05875
3287	8308	13333	1.37	8.0E-57	4758279	NT	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
3287	8308	13334	1.37	8.0E-57	4758279	NT	z151b12.1 Scores testis NHT Homo sapiens cDNA clone IMAGE:757151 5'
4869	9848	14825	0.81	8.0E-57	BE289916.1	EST_HUMAN	Homo sapiens EphA4 (EPHA4) mRNA
2561	7525	12842	0.97	7.0E-57	7657592	NT	600944440F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960864 5'
2561	7525	12843	0.97	7.0E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
3177	8193	13214	1.16	7.0E-57	7242158	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
3177	8193	13215	1.16	7.0E-57	7242158	NT	Homo sapiens NME7 (NME7), mRNA
3197	8213	13235	0.74	7.0E-57	6005979	NT	Homo sapiens NME7 (NME7), mRNA
3786	8789	13793	2.1	7.0E-57	AF012872.1	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3786	8789	13794	2.1	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
4308	9300		1.78	7.0E-57	AF020503.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
3668	8673	13877	2.42	4.0E-57	AB028898.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
795	5818	10847	1.52	3.0E-57	4507788	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1311	6308		153.33	3.0E-57	AA230279.1	EST_HUMAN	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
2327	7301	12421	1.31	3.0E-57	AA348335.1	EST_HUMAN	nc13107.s1 NCI_CGAP_Prl1 Homo sapiens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN
							P46783 40S RIBOSOMAL PROTEIN S10.;
							EST54770 Hippocampus II Homo sapiens cDNA 5' end

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2631	7591	12703	1.45	3.0E-57	BE676622.1	EST_HUMAN	7f33b10.x1 NCI_CGAP_CELL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2 CE20263 ;
2631	7591	12704	1.45	3.0E-57	BE676622.1	EST_HUMAN	7f33b10.x1 NCI_CGAP_CELL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2 CE20263 ;
3482	8490	13506	1.73	3.0E-57	AF232708.1	NT	Homo sapiens cell-line tsA201a chloride ion current inducer protein 1 (Cin) gene, complete cds
3614	8621		31.12	3.0E-57	AW853964.1	EST_HUMAN	RC3-C10254-110300-027-410 C10254 Homo sapiens cDNA
1471	6468	11526	1.55	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1471	6468	11527	1.55	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
2337	7311	12432	1.04	2.0E-57	BE172528.1	EST_HUMAN	MRO-HT0559-010400-009-110 HT0559 Homo sapiens cDNA
3354	8362		3.62	2.0E-57	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3474	8482	13501	0.68	2.0E-57	R07702.1	EST_HUMAN	ye98h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
3474	8482	13502	0.68	2.0E-57	R07702.1	EST_HUMAN	ye98h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
3828	8630	13837	0.83	2.0E-57	BE073264.1	EST_HUMAN	MRO-BT0551-060300-103-b03 BT0551 Homo sapiens cDNA
4063	9057	14044	1.05	2.0E-57	AA018299.1	EST_HUMAN	ze40c06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361450 5'
4063	9057	14045	1.05	2.0E-57	AA018299.1	EST_HUMAN	ze40c06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361450 5'
4379	9370	14349	8.08	2.0E-57	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2170	7149	12266	1.48	1.0E-57	AW503208.1	EST_HUMAN	U1-HF-BNO-ekt-g-07-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
584	5615		1.9	8.0E-58	BE868715.1	EST_HUMAN	601445948F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850211 5'
646	5674	10879	4.07	8.0E-58	AI798376.1	EST_HUMAN	t34b07.x1 NCI_CGAP_OY23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
646	5674	10880	4.07	8.0E-58	AI798376.1	EST_HUMAN	t34b07.x1 NCI_CGAP_OY23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
1820	6810	11802	1.74	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
1820	6810	11803	1.74	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
2906	7925		2.78	8.0E-58	7706132	NT	Homo sapiens DHG1 protein (LOC51304), mRNA
2192	7171	12292	0.98	6.0E-58	BE395061.1	EST_HUMAN	601309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
2314	7289	12410	10.37	6.0E-58	AU130589.1	EST_HUMAN	AU130589 NT2RP3 Homo sapiens cDNA clone N72RP3001283 5'
2831	7951	12870	0.94	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
2831	7951	12871	0.94	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
298	5355	10387	3.24	5.0E-58	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
700	5724	10740	6.5	5.0E-58	BE763984.1	EST_HUMAN	RC4-NT0057-160600-016-b05 NT0057 Homo sapiens cDNA
1175	6178	11213	3.84	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-907 UM0043 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1175	6178	11214	3.64	5.0E-58	AW767948.1	EST_HUMAN	CM3-UM0043-240300-127-607 UM0043 Homo sapiens cDNA
1176	6178	11213	2.81	5.0E-58	AW767948.1	EST_HUMAN	CM3-UM0043-240300-127-607 UM0043 Homo sapiens cDNA
1176	6178	11214	2.81	5.0E-58	AW767948.1	EST_HUMAN	CM3-UM0043-240300-127-607 UM0043 Homo sapiens cDNA
3249	8262	13263	9.15	5.0E-58	AA888183.1	EST_HUMAN	o98e07.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1603908 3'
4136	9131	14114	0.98	5.0E-58	AI636745.1	EST_HUMAN	ts89e07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2238468 3' similar to SW.PRO2_ACACA P19984 PROFILIN II;
372	5421	10435	8.26	4.0E-58	4502302	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O) mRNA
788	5809	10839	1.73	4.0E-58	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
1440	8437	11484	1.06	4.0E-58	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component), Christmas disease, hemophilia B) (F9) mRNA
2559	7524	12840	2.19	4.0E-58	U36251.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 3
3655	8661	13666	1.09	4.0E-58	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
333	5385		1.23	3.0E-58	R17879.1	EST_HUMAN	y810e02.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31893 5'
1368	6363	11412	1.98	3.0E-58	4758981	NT	Homo sapiens peptide YY (PYY) mRNA
3105	8121	13138	3.33	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
3105	8121	13139	3.33	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
926	5943	10977	7.87	2.0E-58	AF068624.1	NT	Homo sapiens 5-aminolevulinate synthase 2 (ALAS2) gene, complete cds
1271	8269		27.01	2.0E-58	BE208532.1	EST_HUMAN	be08b07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X69391 60S RIBOSOMAL PROTEIN L6 (HUMAN); gb:X81987 M.musculus mRNA for TAX responsive element binding protein (MOUSE);
712	5736	10752	0.84	1.0E-58	M65134.1	NT	Human complement component C5 mRNA, 3' end
1051	6060	11089	9.81	1.0E-58	6274549	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1, beta subcomplex, 9 (22kD, B22) (NDUFB9), mRNA
1307	6305	11352	1.04	1.0E-58	AW957182.1	EST_HUMAN	EST389262 MAGe resequences, MAGD Homo sapiens cDNA
1307	6305	11353	1.04	1.0E-58	AW957182.1	EST_HUMAN	EST389252 MAGe resequences, MAGD Homo sapiens cDNA
1373	6370	11419	3.35	1.0E-58	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1824	6921	11689	1.46	1.0E-58	BE466132.1	EST_HUMAN	hy10f08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3186935 3'
2582	7545	12659	0.96	1.0E-58	AF217514.1	NT	Homo sapiens uncharacterized bone marrow protein BM038 mRNA, complete cds
2730	7687	12801	1.98	1.0E-58	4759169	NT	Homo sapiens sterol regulatory element binding transcription factor 2 (SREBF2) mRNA
4811	9795	14778	5.66	1.0E-58	AI141063.1	EST_HUMAN	oz43h01.x1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1678129 3'
2168	7147	12264	69.17	8.0E-59	4507378	NT	Homo sapiens TATA box binding protein (TBP) mRNA
177	7714		2.96	6.0E-59	BF035327.1	EST_HUMAN	601458631F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1715	8710	11786	9.16	5.0E-59	AW157281.1	EST_HUMAN	au83h05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to TR:O75786 O75786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.;
1715	6710	11787	9.16	5.0E-59	AW157281.1	EST_HUMAN	au83h05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to TR:O75786 O75786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.;
3054	8071	13081	6.88	5.0E-59	AI807484.1	EST_HUMAN	wf48c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358836 3'
4523	9513	14498	9.33	5.0E-59	X83497.1	NT	H sapiens DNA for ZNF80-linked ERV9 long terminal repeat
785	5806	10837	2.84	4.0E-59	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
1218	6217	11258	0.67	4.0E-59	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1218	6217	11259	0.67	4.0E-59	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
5017	9888	14964	0.96	4.0E-59	AI890847.1	EST_HUMAN	ws32e12.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2498926 3'
10	6090		4.74	3.0E-59	AW895624.1	EST_HUMAN	EST377682 MAGI resequences, MAGI Homo sapiens cDNA
225	5287	10285	4.43	3.0E-59	7662247	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
1672	6668	11743	8.3	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
1672	6668	11744	8.3	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2071	7053	12162	5.59	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2071	7053	12163	5.59	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2697	7779	12769	0.98	3.0E-59	AF232299.1	NT	Homo sapiens NF1-2 pseudogene, exon 17
3056	8073	13085	3.67	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3056	8073	13086	3.67	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3735	8739	13738	1.33	3.0E-59	4508044	NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA
4547	9536	14523	1.09	3.0E-59	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4693	9678	14662	1.64	3.0E-59	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
4884	9863		0.92	3.0E-59	M95961.1	NT	Human prothormone converting enzyme (NEC2) gene, exon 2
162	5228		37.68	1.0E-59	BE298411.1	EST_HUMAN	601176757F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531927 5'
2544	7509		2.32	1.0E-59	AA748468.1	EST_HUMAN	ca56h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309029 3' similar to TR:Q13537
754	5776	10803	2.17	8.0E-60	AW977845.1	EST_HUMAN	Q13537 MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
1443	6440	11497	8.32	8.0E-60	4759159	NT	EST389849 MAGI resequences, MAGI Homo sapiens cDNA
2107	7087	12201	1.59	8.0E-60	5174656	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA
2107	7087	12202	1.59	8.0E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
745	5768	10794	33.65	7.0E-60	AF055066.1	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
746	5768	10794	109.11	7.0E-60	AF055066.1	NT	Homo sapiens MHC class 1 region

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
805	5828	10856	1.3	7.0E-60	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RE), mRNA
2070	7052	12161	1.23	7.0E-60	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
2712	7668	12782	0.98	7.0E-60	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
4055	9049	14037	4.26	7.0E-60	4505488	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
2114	7094	12208	1.15	6.0E-60	BE984874.2	EST_HUMAN	601658751R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886069 3'
82	5159	10169	0.96	5.0E-60	AB07917.1	EST_HUMAN	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
82	5159	10170	0.96	5.0E-60	AB07917.1	EST_HUMAN	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
2173	7152	12271	1.15	4.0E-60	AW503208.1	EST_HUMAN	UI-HF-BNO-akt-g-07-Q-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2173	7152	12272	1.15	4.0E-60	AW503208.1	EST_HUMAN	UI-HF-BNO-akt-g-07-Q-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2903	7922		1.51	4.0E-60	AA289037.1	EST_HUMAN	EST11498 Uterus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol
1822	6812	11805	3.27	3.0E-60	BE562611.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3680395 5'
1822	6812	11806	3.27	3.0E-60	BE562611.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3680395 5'
1832	6822		9.77	3.0E-60	6031190	NT	Homo sapiens prohibitin (PHB) mRNA
4335	9326	14311	1.67	3.0E-60	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
31	5111	10097	1.22	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1389	6386	11451	6.79	2.0E-60	Z11694.1	NT	H. sapiens 41kDa protein kinase related to rat ERK2
1683	6679	11752	1.46	2.0E-60	M24603.1	NT	Human bcr protein mRNA, 5' end
1692	6688	11763	1.24	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
2532	7497	12617	1.04	2.0E-60	7657229	NT	Homo sapiens interleukin 17 receptor (IL17R), mRNA
3498	8506	13521	0.82	2.0E-60	4757867	NT	Homo sapiens v-rat murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
3817	8819	13826	0.8	2.0E-60	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
518	5553	10556	1	1.0E-60	BE178586.1	EST_HUMAN	PM3-HT0605-270200-001-e06 HT0605 Homo sapiens cDNA
3806	8809	13815	1.97	1.0E-60	AU143389.1	EST_HUMAN	AU143389 Y79AA1 Homo sapiens cDNA clone Y79AA1001854 5'
4789	9783	14766	1.67	1.0E-60	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1082	6089	11118	2.92	9.0E-61	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
2599	7581	12678	1.72	8.0E-61	AW006478.1	EST_HUMAN	w05b10.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2506555 3'
2599	7561	12679	1.72	8.0E-61	AW006478.1	EST_HUMAN	w05b10.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2506555 3'
2880	7899		2.34	8.0E-61	X57147.1	NT	Human endogenous retrovirus pHIE.1 (ERV9)
128	5195	10209	1.8	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
128	5195	10210	1.8	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
4823	5195	10209	2.92	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
4823	5195	10210	2.92	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
263	5322	10331	4.42	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
802	5823	10853	2.26	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1301	6289	11345	12.89	6.0E-61	AF119860.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1609	6605	11668	2.82	6.0E-61	AA596033.1	EST_HUMAN	nm69h09.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897 3'
2068	7050	12158	0.95	6.0E-61	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
3234	8249	13270	13.67	6.0E-61	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
358	5408	10420	0.86	5.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1639	6636	11706	3.51	5.0E-61	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
2865	7983	12997	2.15	5.0E-61	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3125	8141	13162	1.7	5.0E-61	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3874	8875		1.66	5.0E-61	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4843	5408	10420	1.16	5.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
495	5531	10538	1.33	2.0E-61	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
1193	6194	11231	3.21	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1193	6194	11232	3.21	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1628	6623	11692	1.75	2.0E-61	NG3039.1	EST_HUMAN	yw53d11.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:246453 3' similar to gb:L25444.60S RIBOSOMAL PROTEIN L35A (HUMAN);
2570	7533		1.36	2.0E-61	N93937.1	EST_HUMAN	yv03f11.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270189 5'
432	5470		0.75	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
784	5785	10814	1.16	1.0E-61	5453828	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L) mRNA
1732	6727		0.96	1.0E-61	U32657.1	NT	Human polymorphic trinucleotide repeat in X-linked retinitis pigmentosa (RP3) gene region
1821	6811	11804	4.18	1.0E-61	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
2134	7114	12227	1.82	1.0E-61	AW827281.1	EST_HUMAN	xn11b08.y1 NCI_CGAP_Li5 Homo sapiens cDNA clone IMAGE:2683369 5' similar to contains element
2761	7782	12807	2.42	1.0E-61	BE386363.1	EST_HUMAN	MSR1 repetitive element;
3291	8302	13328	0.73	1.0E-61	7662319	NT	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
4317	9309	14294	0.75	1.0E-61	4759249	NT	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
4317	9309	14295	0.75	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4708	9693	14676	9.13	1.0E-61	AW288181.1	EST_HUMAN	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4708	9693	14677	9.13	1.0E-61	AW288181.1	EST_HUMAN	UI-H-BW0-aj1-b-08-0-UJ.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4420	9410	14398	0.92	8.0E-62	AA830420.1	EST_HUMAN	UI-H-BW0-aj1-b-08-0-UJ.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
							oc66h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SW:POL_MLVK
							P31795 POL POLYPROTEIN;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1090	6097	11126	1.09	7.0E-62	AV714334.1	EST_HUMAN	AV714334 DCB Homo sapiens cDNA clone DCBAMJ08 5'
3427	8435	13461	0.93	7.0E-62	P17480	SWISSPROT	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1)
2930	7949		1.58	6.0E-62	U09410.1	NT	(AUTOANTIGEN NOR-90)
3300	8311		4.7	6.0E-62	11418255	NT	Human zinc finger protein ZNF131 mRNA, partial cds
413	5450	10470	3.65	5.0E-62	A1950528.1	EST_HUMAN	Homo sapiens CGI-58 protein (CGI-58), mRNA
2341	7315	12435	3.43	6.0E-62	AJ271735.1	NT	w51e07.x1 NCL_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN
2341	7315	12436	3.43	6.0E-62	AJ271735.1	NT	Q08379 GOLGIN-85; contains element MER22 repetitive element
2515	7483	12599	0.98	5.0E-62	U39487.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2515	7483	12600	0.98	5.0E-62	U39487.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3334	8344	13362	2.46	5.0E-62	4506758	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
4201	9194	14176	1.82	5.0E-62	AA431093.1	EST_HUMAN	Human xanthine dehydrogenase/oxidase mRNA, complete cds
4427	9417		1.12	5.0E-62	AW905887.1	EST_HUMAN	Human xanthine dehydrogenase/oxidase mRNA, complete cds
830	5850	10887	5.18	4.0E-62	AW161479.1	EST_HUMAN	Homo sapiens tyrosine receptor 3 (RYR3) mRNA
830	5850	10888	5.18	4.0E-62	AW161479.1	EST_HUMAN	zw78e09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT
831	5850	10887	3.63	4.0E-62	AW161479.1	EST_HUMAN	P47245 NARDILYSIN
831	5850	10888	3.63	4.0E-62	AW161479.1	EST_HUMAN	P47245 NARDILYSIN
831	5850	10888	3.63	4.0E-62	AW161479.1	EST_HUMAN	RC5-NN1089-100500-021-H03 NN1089 Homo sapiens cDNA
2389	7360	12482	4.43	4.0E-62	A1827600.1	EST_HUMAN	RC5-NN1089-100500-021-H03 NN1089 Homo sapiens cDNA
2389	7360	12483	4.43	4.0E-62	A1827600.1	EST_HUMAN	RC5-NN1089-100500-021-H03 NN1089 Homo sapiens cDNA
3315	8328		7.88	4.0E-62	4557887	NT	RC5-NN1089-100500-021-H03 NN1089 Homo sapiens cDNA
5023	9984	14987	0.97	4.0E-62	4758323	NT	RC5-NN1089-100500-021-H03 NN1089 Homo sapiens cDNA
73	5151	10160	1.46	3.0E-62	4557794	NT	RC5-NN1089-100500-021-H03 NN1089 Homo sapiens cDNA
2972	7990	13003	0.71	3.0E-62	AB040909.1	NT	RC5-NN1089-100500-021-H03 NN1089 Homo sapiens cDNA
2972	7990	13004	0.71	3.0E-62	AB040909.1	NT	RC5-NN1089-100500-021-H03 NN1089 Homo sapiens cDNA
3615	8622	13630	8.12	3.0E-62	X52858.1	NT	RC5-NN1089-100500-021-H03 NN1089 Homo sapiens cDNA
1211	6211	11251	2.89	2.0E-62	AL163284.2	NT	RC5-NN1089-100500-021-H03 NN1089 Homo sapiens cDNA

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1027	6037	11069	1.58	1.0E-62	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1512	6510	11587	15.3	1.0E-62	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
1763	6755	11840	1.92	1.0E-62	AA625207.1	EST_HUMAN	af70611.1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1
2844	7864	12882	1.18	1.0E-62	AL039044.1	EST_HUMAN	CE03453
3339	8348		2.49	1.0E-62	AB040811.1	NT	DKFZp566F104.1 566 (synonym: htkd2) Homo sapiens cDNA clone DKFZp566F104 5'
4395	9386	14369	1.63	1.0E-62	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
4956	9933	14911	0.88	1.0E-62	AA148822.1	EST_HUMAN	z06b08.1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:491511 5' similar to
336	5388	10395	1.82	9.0E-63	AW816405.1	EST_HUMAN	SW:C561_BOVIN P10897 CYTOCHROME B561
2284	7260		1.09	9.0E-63	C18159.1	EST_HUMAN	QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
3928	8928	13918	9.26	9.0E-63	AB002348.2	NT	C18159 Human placenta cDNA (TFujikawa) Homo sapiens cDNA clone GEN-558C10 5'
3928	8928	13919	9.26	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
							Homo sapiens mRNA for KIAA0350 protein, partial cds
5058	10028	14895	4.71	9.0E-63	AA015938.1	EST_HUMAN	z631d08.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360591 5' similar to
							SW:UN13_CAEEL P2715 PHORBOL ESTER/DIACYL GLYCEROL-BINDING PROTEIN UNC-13. [1]
2282	7258	12376	2.39	8.0E-63	4557734	NT	Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2313	7288	12409	5.14	8.0E-63	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3378	8387	13408	4.89	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3378	8387	13408	4.89	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4143	9138	14122	3.27	8.0E-63	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
916	5932		1.84	7.0E-63	AI872137.1	EST_HUMAN	wn55g11.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439908 3'
3247	8260	13282	0.71	4.0E-63	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3719	8723	13722	2.01	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
3719	8723	13723	2.01	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
1895	6883	11975	2.67	3.0E-63	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
2706	7663	12774	1.34	3.0E-63	J00310.1	NT	Human Met-RNA-1 gene 1
2748	6219	11262	10.16	3.0E-63	6005963	NT	Homo sapiens zinc finger protein 144 (ZNF144), mRNA
191	5255	10267	2.47	2.0E-63	U07804.1	NT	Human DNA topoisomerase I mRNA, partial cds
188	5262	10275	1.85	2.0E-63	4885226	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
							Homo sapiens glutamate-cysteine ligase (germme-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA
494	5530		1.36	2.0E-63	4557624	NT	
816	5837	10872	4.72	2.0E-63	7557042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
1533	6531	11591	1.52	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1533	6531	11592	1.52	2.0E-63	AB030398.1	NT	Homo sapiens RHCE mRNA for Rh blood OE group antigen polypeptide, complete cds
1726	6724	11802	3	2.0E-63	BE410739.1	EST_HUMAN	601301627F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638103 5'
3083	8099	13114	1.58	2.0E-63	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3212	8227	13249	2.2	2.0E-63	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
3809	8812	13818	1.4	2.0E-63	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
4716	9701	14687	1.23	2.0E-63	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4216	9209	14188	3.33	1.0E-63	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
4216	9209	14189	3.33	1.0E-63	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
1029	6039		9.14	8.0E-64	BE280798.1	EST_HUMAN	601155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5'
3451	8459		0.9	7.0E-64	BE394321.1	EST_HUMAN	601311456F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5'
4593	9581	14570	3.25	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOPT) mRNA
4593	9581	14571	3.25	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOPT) mRNA
1684	6680	11753	5.45	6.0E-64	A1651992.1	EST_HUMAN	wb51e07.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
1684	6680	11754	5.45	6.0E-64	A1651992.1	EST_HUMAN	wb51e07.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
3049	8068	13074	5.09	6.0E-64	AW026445.1	EST_HUMAN	w13e03.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
3049	8068	13075	5.09	6.0E-64	AW026445.1	EST_HUMAN	w13e03.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
810	5831	10863	3.24	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
810	5831	10864	3.24	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1318	6316	11364	2.38	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1397	6394	11448	1.35	5.0E-64	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1397	6394	11449	1.35	5.0E-64	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1673	6669	11745	1.5	6.0E-64	U89358.1	NT	Human (3)mbt protein homolog mRNA, complete cds
2753	8447	11506	4.17	5.0E-64	7662205	NT	Homo sapiens KIAA0818 gene product (KIAA0818), mRNA
2753	8447	11507	4.17	5.0E-64	7662205	NT	Homo sapiens KIAA0818 gene product (KIAA0818), mRNA
3852	8854	13859	8.23	5.0E-64	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
3852	8854	13859	8.23	5.0E-64	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
3898	8868	13972	1.02	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
2135	7116	12228	3.23	3.0E-64	C18895.1	EST_HUMAN	C18895 Human placenta cDNA (Tfujware) Homo sapiens cDNA clone GEN-589E02 5'
3359	8387	13385	1.37	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
3359	8387	13386	1.37	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
1072	6090	11111	1.32	2.0E-64	AA609940.1	EST_HUMAN	af08d08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031151 3'

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1374	6371	11420	5.42	2.0E-64	4757701	NT	Homo sapiens eIF4E-like cap-binding protein (4EHP) mRNA
2454	7424		1.92	2.0E-64	A1927030.1	EST_HUMAN	wo37b01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462281 3' similar to contains element L1 repetitive element ;
2459	7428	12544	2.92	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2459	7428	12545	2.92	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3067	8083	13097	0.91	2.0E-64	4504088	NT	Homo sapiens glutamyl-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
256	5316	10325	1.58	1.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1741	6736	11812	51.93	1.0E-64	A1928419.1	EST_HUMAN	eu60c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519136 3' similar to gb:U21696 cds1 PROTHYMOSIN ALPHA (HUMAN); contains element MSR1 repetitive element ;
2942	7961	12981	0.81	1.0E-64	4507334	NT	Homo sapiens synapjanin 1 (SYNJ1), mRNA
3432	8440	13467	5	1.0E-64	AF106779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds; and L-type calcium channel $\alpha 2$
3503	8511	13525	1.46	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3503	8511	13528	1.46	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3805	8808	13814	0.87	1.0E-64	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
2214	7191	12312	1.09	9.0E-65	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2214	7191	12313	1.09	9.0E-65	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
1039	6049	11079	3.17	6.0E-65	AV721898.1	EST_HUMAN	AV721898 HTB Homo sapiens cDNA clone HTBBZC08 5'
1880	6889		48.55	6.0E-65	AA550929.1	EST_HUMAN	ribosomal protein L32 (HUMAN);
625	5652	10656	0.96	6.0E-65	AF084604.1	NT	Homo sapiens KE03 protein mRNA, partial cds
1335	6333	11381	1.94	5.0E-65	7661951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
1335	6333	11382	1.94	5.0E-65	7661951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
3181	8197	13220	1.88	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3181	8197	13221	1.88	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
163	5257	10270	3.82	4.0E-65	AL120419.1	EST_HUMAN	DKFZp761G108_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108 5'
736	5759	10781	1.07	4.0E-65	A1266468.1	EST_HUMAN	qm46a01.x1 Soares_placenta_8to9weeks_2NbHP8t9w Homo sapiens cDNA clone IMAGE:1891800 3'
736	5759	10782	1.07	4.0E-65	A1266468.1	EST_HUMAN	qm46a01.x1 Soares_placenta_8to9weeks_2NbHP8t9w Homo sapiens cDNA clone IMAGE:1891800 3'
1062	6070	11102	6.88	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
1455	8452	11511	18.94	4.0E-65	4506636	NT	Homo sapiens ribosomal protein L34 (RPL34) mRNA

Table 4
Single Exon Probes Expressed In HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2275	7251	12388	3.52	4.0E-65	BE221469.1	EST_HUMAN	hu25e04.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'
2275	7251	12389	3.52	4.0E-65	BE221469.1	EST_HUMAN	hu25e04.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'
3845	8847	13855	1.07	4.0E-65	AW693185.1	EST_HUMAN	RC2-BN0033-160200-013-a03 BN0033 Homo sapiens cDNA
98	5174	10185	1.82	3.0E-65	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
97	5174	10185	1.75	3.0E-65	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1212	7699		12.12	3.0E-65	X78932.1	NT	H. sapiens HZF9 mRNA for zinc finger protein
1627	6524	11581	1.55	3.0E-65	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1787	6778	11871	1.62	3.0E-65	A100692.1	EST_HUMAN	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element MSR1 repetitive element;
2821	7940	12956	0.89	3.0E-65	D87078.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
3203	8218	13241	0.83	3.0E-65	4504950	NT	Homo sapiens laminin, beta 1 (LAMB1), mRNA
3638	8644	13650	1.17	3.0E-65	A100692.1	EST_HUMAN	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element MSR1 repetitive element;
4515	9505	14485	1.45	3.0E-65	6912385	NT	Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA
3320	8330	13351	6.2	2.0E-65	BF680294.1	EST_HUMAN	602155062F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285956 5'
89	5166		1.12	1.0E-65	BF125544.1	EST_HUMAN	601763488F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026501 5'
534	5569	10572	1.79	1.0E-65	7657495	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
1989	6974	12078	1.12	1.0E-65	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
3280	8301	13327	0.79	1.0E-65	BE466881.1	EST_HUMAN	hz24a09.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:3208888 3'
3892	8892	13890	1.89	1.0E-65	4504082	NT	Homo sapiens glypican 4 (GPC4) mRNA
3892	8892	13891	1.89	1.0E-65	4504082	NT	Homo sapiens glypican 4 (GPC4) mRNA
4084	8078	14066	3.43	1.0E-65	AW028340.1	EST_HUMAN	wx08e09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
4084	8078	14067	3.43	1.0E-65	AW028340.1	EST_HUMAN	wx08e09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
70	5149	10156	1.28	9.0E-66	AL160311.1	NT	Novel human gene mapping to chromosome 22
70	5149	10157	1.28	9.0E-66	AL160311.1	NT	Novel human gene mapping to chromosome 22
1336	6334	11383	2.47	9.0E-66	5031980	NT	Homo sapiens 26S proteasome-associated ped1 homolog (POH1) mRNA
1336	6334	11384	2.47	9.0E-66	5031980	NT	Homo sapiens 26S proteasome-associated ped1 homolog (POH1) mRNA
1453	6450		3.8	9.0E-66	M87299.1	NT	Human transposon-like element, partial
4553	9541	14526	0.96	9.0E-66	AL137163.1	NT	Novel human gene mapping to chromosome X
4240	8234	14216	1.02	6.0E-66	A1924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP.F15G9.4A CE18595;
4240	8234	14217	1.02	6.0E-66	A1924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP.F15G9.4A CE18595;

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4240	9234	14218	1.02	6.0E-66	A1924653.1	EST_HUMAN	wn57h07.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A CE18595;
1349	6346	11397	1.88	5.0E-66	BE084410.1	EST_HUMAN	RC4-BT0311-141199-011-h08 BT0311 Homo sapiens cDNA
4939	8916	14895	0.81	5.0E-66	BE898644.1	EST_HUMAN	601681592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951791 5'
4939	8916	14896	0.81	5.0E-66	BE898644.1	EST_HUMAN	601681592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951791 5'
782	5803	10833	2.44	4.0E-66	6879816	NT	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA
1698	6693	11769	1.24	4.0E-66	AW897798.1	EST_HUMAN	RC1-NN0063-100500-022-e02 NN0063 Homo sapiens cDNA
2217	7194	12316	2.12	4.0E-66	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2403	7374		2.81	4.0E-66	AJ223394.1	NT	Homo sapiens germ-line DNA upstream of Jkappa locus
4638	8623		4.36	4.0E-66	8835487	NT	Human endogenous retrovirus, complete genome
1402	6399	11455	34.87	3.0E-66	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1402	6399	11456	34.87	3.0E-66	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1938	6922	12020	1.02	3.0E-66	N55323.1	EST_HUMAN	yz27g12.r1 Soares_multiple_sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2; [2] PIR:B56612;
1936	6922	12021	1.02	3.0E-66	N55323.1	EST_HUMAN	yz27g12.r1 Soares_multiple_sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2; [2] PIR:B56612;
1938	6922	12022	1.02	3.0E-66	N55323.1	EST_HUMAN	yz27g12.r1 Soares_multiple_sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2; [2] PIR:B56612;
2635	7595	12708	2.42	3.0E-66	11141880	NT	Homo sapiens TGF(beta)-induced transcription factor 2 (TGIF2), mRNA
3043	8060	13089	7.45	3.0E-66	7662223	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
52	5133	10128	1.38	2.0E-66	7657334	NT	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA
52	5133	10128	1.38	2.0E-66	7657334	NT	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA
419	5077	10061	1.14	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
419	5077	10062	1.14	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
1791	6782	11874	2.52	2.0E-66	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2905	7924	12943	0.88	2.0E-66	XG5859.1	NT	H. sapiens pseudogene for the low affinity IL-8 receptor
3879	8684	13686	0.82	2.0E-66	AL117233.1	NT	Novel human gene mapping to chromosome 1
4137	9132	14115	0.91	2.0E-66	8923768	NT	Homo sapiens histone deacetylase 8 (HDAC8 gene) (HSA277724), mRNA
4521	9511	14495	39.41	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B
4521	9511	14496	39.41	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1644	6840		1.17	1.0E-66	BE887173.1	EST_HUMAN	601508376F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3809831 5'
2823	7844	12863	1.49	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADCO7 5'
2823	7844	12864	1.49	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADCO7 5'
4260	7844	12863	3.88	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADCO7 5'
4260	7844	12864	3.88	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADCO7 5'
379	5454	10471	4.95	7.0E-67	AW162232.1	EST_HUMAN	au76402.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1363	6360	11410	2.15	7.0E-67	AA383416.1	EST_HUMAN	EST86812 Testis I Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid ZK353
1523	6520	11576	1.98	7.0E-67	W85947.1	EST_HUMAN	zh56805.r1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1523	6520	11577	1.98	7.0E-67	W85947.1	EST_HUMAN	zh56805.r1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1882	6987	12072	1.31	7.0E-67	7657243	NT	Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
1882	6987	12073	1.31	7.0E-67	7657243	NT	Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
2738	5454	10471	4.77	7.0E-67	AW162232.1	EST_HUMAN	au76402.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
555	5589	10590	1.53	6.0E-67	X68998.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
787	5808	10838	2.36	6.0E-67	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
1254	6252	11293	1.35	6.0E-67	Y14320.1	NT	Homo sapiens PMP69 gene, exons 3,4,5,6 & 7
3095	8111	13129	1.52	6.0E-67	4506434	NT	Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA
3353	8361	13377	1.44	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
3353	8361	13378	1.44	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
4567	9555	14542	3.45	6.0E-67	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4567	9555	14543	3.45	6.0E-67	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4805	9789		0.86	6.0E-67	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
5012	9983	14958	1.01	6.0E-67	AF016898.1	NT	Homo sapiens B-ATF gene, complete cds
5012	9983	14959	1.01	6.0E-67	AF016898.1	NT	Homo sapiens B-ATF gene, complete cds
3150	8168	13186	2.02	5.0E-67	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TORBV7S3A2 to TORBV12S2 region
1308	6306	11354	1.2	4.0E-67	R90819.1	EST_HUMAN	yn02d11.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:167263 5'
2741	5554	10859	1.65	3.0E-67	AA333768.1	EST_HUMAN	EST137803 Embryo, 9 week Homo sapiens cDNA 5' end
3371	8378	13399	1.01	3.0E-67	BE064410.1	EST_HUMAN	RC4-BT0311-141189-011-h08 BT0311 Homo sapiens cDNA
4555	9543	14528	3.04	3.0E-67	AW869159.1	EST_HUMAN	MR3-SN0066-040500-008-f01 SN0068 Homo sapiens cDNA
188	5252	10263	1.1	2.0E-67	BE348354.1	EST_HUMAN	hw16g09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183136 3' similar to WP.F23H11.9 CE09617;
835	5854	10894	5.38	2.0E-67	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1088	6095		2.11	2.0E-67	AF167460.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4
1845	6834	11924	1.28	2.0E-67	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2805976 5' similar to TR:O94892 O94892 KIAA0798 PROTEIN. ;
1845	6834	11925	1.28	2.0E-67	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2805976 5' similar to TR:O94892 O94892 KIAA0798 PROTEIN. ;
2178	7158	12277	1.81	2.0E-67	11422946	NT	Homo sapiens hypothetical protein dJ462O23.2 (DJ462O23.2), mRNA
2178	7158	12278	1.81	2.0E-67	11422946	NT	Homo sapiens hypothetical protein dJ462O23.2 (DJ462O23.2), mRNA
2323	7287	12419	1.29	2.0E-67	AF309561.1	NT	Homo sapiens KRAB zinc finger protein ZFOR mRNA, complete cds
2364	7338	12455	2.28	2.0E-67	4758785	NT	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA
3387	8395	13419	3.66	2.0E-67	AA625755.1	EST_HUMAN	zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
3896	8896	13894	2.87	2.0E-67	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
251	5311	10322	2.94	1.0E-67	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
698	5722	10738	2.16	1.0E-67	AA702784.1	EST_HUMAN	z69b04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
2111	7091	12205	2.23	8.0E-68	BE870732.1	EST_HUMAN	601448558f1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5'
3778	8781	13784	4.83	8.0E-68	AA209456.1	EST_HUMAN	zq82h10.r1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW_SAV_SULAC Q07590 SAV PROTEIN. ;
3778	8781	13785	4.83	8.0E-68	AA209456.1	EST_HUMAN	zq82h10.r1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW_SAV_SULAC Q07590 SAV PROTEIN. ;
1851	6840		1.93	8.0E-68	AW503842.1	EST_HUMAN	UI-HF-BN0-alc-c-07-0-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078924 5'
808	5830	10861	3.82	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
808	5830	10862	3.82	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
2707	7664	12775	1.09	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3074	8080	13104	3.02	5.0E-68	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
4057	9051		0.68	5.0E-68	4926967	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
4363	9354	14333	0.66	5.0E-68	AL157845.1	EST_HUMAN	DKFZp547D207_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D207 5'
2456	7428	12540	1.15	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
2456	7428	12541	1.15	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
4816	9800		16.14	4.0E-68	P04406	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
3577	8584	13589	7.2	3.0E-68	AF236082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
2791	10054		39.36	2.0E-68	D00522.1	NT	Cricetus longicaudatus mRNA for EF-1 alpha, complete cds
3915	8915	13908	0.68	2.0E-68	BE675766.1	EST_HUMAN	7f15f02.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3294747 3' similar to TR:O80828 O80828 HYPOTHETICAL 88.3 KD PROTEIN. ;
4543	9532	14520	1.64	2.0E-68	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
78	5155	10166	0.94	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
284	5351	10364	11.12	1.0E-68	AW816405.1	EST_HUMAN	QV4-ST0234-181189-037-405 ST0234 Homo sapiens cDNA
2190	7169	12289	1.74	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2190	7169	12290	1.74	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
3903	8903	13901	0.97	1.0E-68	BE298032.1	EST_HUMAN	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5'
4901	8880	14849	1.18	1.0E-68	BE298032.1	EST_HUMAN	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5'
20	5100	10083	7.87	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
20	5100	10084	7.87	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1011	6021	11050	2.59	9.0E-69	5031880	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1011	6021	11051	2.59	9.0E-69	5031880	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
5035	10008	14977	0.94	9.0E-69	4507164	NT	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
3302	8313		1.28	8.0E-69	AJ237444.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
516	5551		0.99	4.0E-69	AB73630.1	EST_HUMAN	wm26h1.1 x1 NCI CGAP_U4 Homo sapiens cDNA clone IMAGE:2437125 3'
385	5460	10478	5.07	3.0E-69	BE258012.1	EST_HUMAN	601110371F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351352 5'
608	5635	10636	2.03	3.0E-69	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
1524	6521		1.63	3.0E-69	T80514.1	EST_HUMAN	y08a02.1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24880 5' similar to SP:A48836
4804	9788	14771	0.97	3.0E-69	AB037732.1	NT	A48836 SPEGF III-EGF REPEAT-CONTAINING FIBROCELL-LIKE PROTEIN - SEA URCHIN ;
4871	8965	13954	1.66	3.0E-69	AF765888.1	EST_HUMAN	Homo sapiens mRNA for KIAA1311 protein, partial cds
129	5438	10457	2.01	2.0E-69	AF160252.1	NT	wh86g08.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385758 3'
129	5438	10458	2.01	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
402	5438	10457	5.22	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
402	5438	10458	5.22	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
1846	6835	11926	2.59	2.0E-69	BE257857.1	EST_HUMAN	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
2770	7781		3.44	2.0E-69	AA431157.1	EST_HUMAN	601109444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3360074 5'
4970	9947	14924	1.2	2.0E-69	4504148	NT	zw71g02.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:781682 5'
4970	9947	14925	1.2	2.0E-69	4504148	NT	Homo sapiens glutamate receptor, metabotropic 8 (GRM8) mRNA
1684	8660	11734	1.7	1.0E-69	AF053768.1	NT	Homo sapiens glutamate receptor, metabotropic 8 (GRM8) mRNA
2270	7766	12363	1.55	8.0E-70	AA230303.1	EST_HUMAN	Rattus norvegicus brain specific cortactin-binding protein CBP80 mRNA, partial cds
4248	9242	14226	2	8.0E-70	L77566.1	NT	nc13d12.1 NCI CGAP_P1 Homo sapiens cDNA clone IMAGE:1008023
1777	6769	11860	4.59	7.0E-70	AI497807.1	EST_HUMAN	Homo sapiens DGS-1 mRNA, 3' end
1777	6769	11861	4.59	7.0E-70	AI497807.1	EST_HUMAN	bm89f01.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3'
1890	6879	11969	2.37	7.0E-70	AA282955.1	EST_HUMAN	bm89f01.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3'
							z15h04.1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713239 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2011	6994		6.81	7.0E-70	5031688	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA
4103	9097	14083	3.55	7.0E-70	4757723	NT	Homo sapiens adenylate cyclase 3 (ADCY3) mRNA
860	5879	10920	4.09	6.0E-70	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2078	7059	12169	4.32	6.0E-70	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
2437	7408	12525	1.12	6.0E-70	8923899	NT	Homo sapiens CMP-N-acetylneuraminic acid synthase (LOC55907), mRNA
2481	7772	12581	1.53	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
2481	7772	12582	1.53	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
1554	6551	11610	3.24	3.0E-70	BE071796.1	EST_HUMAN	RCO-BT0522-071296-011-a12 BT0522 Homo sapiens cDNA
1554	6551	11611	3.24	3.0E-70	BE071798.1	EST_HUMAN	RCO-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA
39	5119	10107	1.16	2.0E-70	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
680	5705	10714	11.75	2.0E-70	N42161.1	EST_HUMAN	Y07a10.1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P29268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
680	5705	10715	11.75	2.0E-70	N42161.1	EST_HUMAN	Y07a10.1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P29268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
695	5719	10737	1.73	2.0E-70	A1246899.1	EST_HUMAN	q651h01.x1 NC1_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004913 3'
1005	6015	11045	2.33	2.0E-70	8923669	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
1165	6168	11202	1.5	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1165	6168	11203	1.5	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1615	6612	11678	1.22	2.0E-70	AA180093.1	EST_HUMAN	zp45h05.r1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:612441 5' similar to TR:G1041293 G1041293 D2085.5 ;
1615	6612	11679	1.22	2.0E-70	AA180093.1	EST_HUMAN	zp45h05.r1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:612441 5' similar to TR:G1041293 G1041293 D2085.5 ;
1703	6698	11774	1.85	2.0E-70	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2256	7233		7.98	2.0E-70	AA054010.1	EST_HUMAN	zf48g04.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTL1A
2415	7396	12506	1.57	2.0E-70	AB011173.1	NT	P03345 GAG POLYPROTEIN ;
3728	8732	13730	1.26	2.0E-70	AL133207.2	NT	Homo sapiens mRNA for KIAA0601 protein, partial cds
3838	8840	13847	1.17	2.0E-70	AJ246003.1	NT	Novel human gene mapping to chromosome X
3936	8935	13928	4.94	2.0E-70	M69181.1	NT	Homo sapiens Spast gene for spastin protein
4069	9063	14051	1.03	2.0E-70	L78810.1	NT	Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds
4069	9063	14052	1.03	2.0E-70	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4069	9063	14052	1.03	2.0E-70	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
3309	8320		3.18	1.0E-70	4507476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2148	7127	12244	14.02	5.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4001	8997	13986	0.87	5.0E-71	AW816405.1	EST_HUMAN	QV4-ST0234-181189-037.05 ST0234 Homo sapiens cDNA
103	5180	10191	0.87	4.0E-71	4507592	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
348	5400	10409	215.31	4.0E-71	AF157626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
348	5400	10410	215.31	4.0E-71	AF157626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2818	7838	12851	1.81	4.0E-71	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4304	9286	14282	7.98	4.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4827	8811	14792	6.12	4.0E-71	7657602	NT	Homo sapiens putative heme-binding protein (SOL), mRNA
1270	8210	11250	16.61	2.0E-71	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
632	5660	10665	1.87	1.0E-71	A077927.1	EST_HUMAN	oy15e03.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1665916 3' similar to contains LOR1.b2 LOR1 repetitive element
927	5944	10978	6.13	1.0E-71	7708281	NT	Homo sapiens neuronal cell death-related protein (LQCS1616), mRNA
1083	6030	11119	4.33	1.0E-71	AF205890.1	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds
1320	6318	11366	8.38	1.0E-71	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4k230) mRNA, complete cds
2029	7012	12120	1.35	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2621	7583	12693	3.09	1.0E-71	7657153	NT	Homo sapiens hairy/enhancer-of-split related with YRPW motif-like (HEYL), mRNA
3422	8430	13456	2.38	1.0E-71	AF119885.1	NT	Homo sapiens inorganic pyrophosphatase mRNA, complete cds
3516	8524	13534	6.34	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3516	8524	13535	5.34	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3563	8570	13575	0.73	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3563	8570	13576	0.73	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3658	8662	13667	1.73	1.0E-71	AF218904.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 19
4345	9338	14318	2.05	1.0E-71	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
4460	9450	14431	1.19	1.0E-71	H23176.1	EST_HUMAN	ym58h10.1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:52525 5'
405	5441	10460	0.74	9.0E-72	A1857635.1	EST_HUMAN	wk95g03.x1 NCL CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705
405	5441	10461	0.74	9.0E-72	A1857635.1	EST_HUMAN	HYPOTHETICAL 38.6 KD PROTEIN, contains Alu repetitive element
3996	8992	13977	1.64	7.0E-72	4501868	NT	wk95g03.x1 NCL CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705
							HYPOTHETICAL 38.6 KD PROTEIN, contains Alu repetitive element
							Homo sapiens acetylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3998	8992	13978	1.54	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
3999	8992	13979	1.54	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
64	5144	10148	2.81	5.0E-72	BF333707.1	EST_HUMAN	QV0-150900-398-811 CS0010 Homo sapiens cDNA
64	5144	10149	2.81	5.0E-72	BF333707.1	EST_HUMAN	QV0-150900-398-811 CS0010 Homo sapiens cDNA
65	5144	10148	18.08	5.0E-72	BF333707.1	EST_HUMAN	QV0-150900-398-811 CS0010 Homo sapiens cDNA
65	5144	10149	18.08	5.0E-72	BF333707.1	EST_HUMAN	QV0-150900-398-811 CS0010 Homo sapiens cDNA
1122	6128		2.73	5.0E-72	L11645.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
4678	9661		1.32	4.0E-72	11034844	NT	Homo sapiens hypothetical protein dJ1057B20.2 (D.J1057B20.2), mRNA
5048	10019	14988	1.07	4.0E-72	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
19	5099	10082	2.48	3.0E-72	5031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
892	5910		1.27	3.0E-72	AA723823.1	EST_HUMAN	ah33a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1310290 3'
1137	6142	11171	11.37	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1137	6142	11172	11.37	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1174	6177	11211	1.12	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1174	6177	11212	1.12	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
3001	8018	13032	12.79	3.0E-72	AJ228043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3205	8220	13242	2.5	3.0E-72	8923548	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
3732	8736	13734	3.01	3.0E-72	S77589.1	NT	TCR V delta 2-C alpha T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction)
4414	9404	14389	3.55	3.0E-72	11416198	NT	[human, precursor B-cell line REH, mRNA Partial, 211 nt]
4621	9606	14593	1.08	3.0E-72	AF167572.1	NT	Homo sapiens hypothetical protein (FLJ11127), mRNA
4621	9606	14594	1.08	3.0E-72	AF167572.1	NT	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds
2022	7005	12110	1.03	1.0E-72	AA846225.1	EST_HUMAN	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds
1433	6430	11486	1.25	9.0E-73	AW374968.1	EST_HUMAN	al83d02.s1 Soares_parallelized_tumor_NHHPA Homo sapiens cDNA clone IMAGE:1387395 3'
1021	6030	11060	3.27	8.0E-73	AW071755.1	EST_HUMAN	MRO-CT0063-071099-002-h11 CT0063 Homo sapiens cDNA
1117	6123	11153	0.98	7.0E-73	8923280	NT	ws55c08.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2501088 3' similar to TR:Q59050
3227	8242	13264	1.84	7.0E-73	AL163206.2	NT	Q59050 HYPOTHETICAL PROTEIN FLJ20309 (FLJ20309), mRNA
4787	9771		1.48	7.0E-73	AL163282.2	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
157	5223		1.71	6.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C082
						NT	Homo sapiens chromosome 21 segment HS21C018

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1321	6319	11367	1.38	3.0E-73	AW843789.1	EST_HUMAN	CM0-CN0044-260100-164-08 CN0044 Homo sapiens cDNA
1825	6815	11909	1.1	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
1825	6815	11910	1.1	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
841	5860	10900	2.37	2.0E-73	AF139897.1	NT	Homo sapiens BASS1 (BASS1) mRNA, partial cds
1806	6893		3.12	2.0E-73	AW888081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
3108	8124	13143	3.89	2.0E-73	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
4311	9303		1.02	2.0E-73	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
1745	6740	11819	2.61	1.0E-73	AU121585.1	EST_HUMAN	AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5'
2413	7384	12503	1.04	1.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
731	5754	10775	1.76	8.0E-74	4557426	NT	Homo sapiens CD39-like 4 (CD39L4) mRNA
1809	6895	11989	2.57	7.0E-74	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
3253	8266	13288	1.22	7.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1105	6112	11143	4	6.0E-74	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
1587	6584	11645	0.92	6.0E-74	AW263177.1	EST_HUMAN	nt78g07.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2700638 3'
2252	7229	12347	53.86	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605463 5'
2252	7229	12348	53.86	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605463 5'
2793	7813	12831	0.97	6.0E-74	AW014039.1	EST_HUMAN	U1-H-B10-aah-h-03-0-UJ.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
2793	7813	12832	0.97	6.0E-74	AW014039.1	EST_HUMAN	U1-H-B10-aah-h-03-0-UJ.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
3631	8637	13842	1.37	6.0E-74	BE048946.1	EST_HUMAN	h154e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
3631	8637	13843	1.37	6.0E-74	BE048946.1	EST_HUMAN	h154e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
4866	9846	14821	1.55	6.0E-74	4758135	NT	Homo sapiens DEAD1H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
4866	9846	14822	1.55	6.0E-74	4758135	NT	Homo sapiens DEAD1H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
894	5912	10951	2.15	5.0E-74	AW020988.1	EST_HUMAN	df17c08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
2630	7590		6.51	5.0E-74	AW362756.1	EST_HUMAN	PMO-CT0289-271099-001-h07 CT0289 Homo sapiens cDNA
277	5335	10348	5.48	4.0E-74	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
842	5881	10901	5.8	4.0E-74	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
1922	6908	12002	1.42	4.0E-74	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1922	6908	12003	1.42	4.0E-74	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2019	7002	12106	5.12	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2019	7002	12107	5.12	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2074	7056	12166	1.18	4.0E-74	AB032994.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
3017	8034	13045	5.03	4.0E-74	AJ008976.1	NT	Homo sapiens PLP gene
3449	8457	13483	0.81	4.0E-74	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3950	8948	13937	1.22	4.0E-74	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4425	9415	14402	1.86	4.0E-74	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569) mRNA
4481	9471	14452	1.19	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
4902	9881	14850	1.02	4.0E-74	4504326	NT	Homo sapiens hydroxycy-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
4902	9881	14851	1.02	4.0E-74	4504326	NT	Homo sapiens hydroxycy-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
5011	9982	14957	0.91	4.0E-74	AB037863.1	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
943	5960	10993	263.61	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
943	5960	10994	263.61	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1156	6160	11194	1.2	2.0E-74	AF020092.1	NT	Human endogenous retrovirus HERV-K-T47D
1225	6224	11270	2.76	2.0E-74	AI950528.1	EST_HUMAN	wx51e07.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN Q06379 GOLGIN-95; contains element MER22 repetitive element
1560	6557	11618	3.33	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
1560	6557	11619	3.33	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
2526	7492	12612	3.99	2.0E-74	AI557280.1	EST_HUMAN	PT2.1_15_G11.r tumor2 Homo sapiens cDNA 3'
4846	9828	14802	2.77	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
4846	9828	14803	2.77	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
4850	9832	14807	3.98	2.0E-74	J02963.1	NT	Human platelet glycoprotein IIb mRNA, 3' end
54	5135	10132	2.92	1.0E-74	7657334	NT	Homo sapiens Mtschaper/NIK-related kinase (MINK), mRNA
335	5387	10394	4.23	1.0E-74	AW816405.1	EST_HUMAN	QV4-ST0234-181198-037-05 ST0234 Homo sapiens cDNA
496	5532	10539	1.19	1.0E-74	8922828	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
503	5538	10544	29.75	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
596	5627	10626	2.36	1.0E-74	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
984	5999	11030	2.04	1.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2165	7144	12262	5	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
3066	8082	13096	3.19	1.0E-74	4756697	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
3822	8824	13831	0.67	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3822	8824	13832	0.67	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3861	8863	13868	4.97	1.0E-74	AL168288.2	NT	Homo sapiens chromosome 21 segment HS21C068
4145	9140	14124	1.12	1.0E-74	BE467769.1	EST_HUMAN	h273h08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213663 3' similar to WP:B0511.12
2573	7538		3.52	8.0E-75	AF176228.1	NT	CE17351;
2257	7234	12352	0.98	6.0E-75	AB17415.1	EST_HUMAN	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
112	5184	10193	3.57	4.0E-75	BE081333.1	EST_HUMAN	wk38a08.x1 NCL_CGAP_P122 Homo sapiens cDNA clone IMAGE:2417654 3' similar to gb:M14123_cds4
456	5493		0.99	4.0E-75	N36757.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN (HUMAN);
1728	6723	11801	1.27	4.0E-75	AW897230.1	EST_HUMAN	QV1-BT0632-210200-078-e02 BT0632 Homo sapiens cDNA
2776	7797	12816	5.17	4.0E-75	BE409464.1	EST_HUMAN	yx80h08.r1 Soares melanocyte 2NbhM Homo sapiens cDNA
3421	8429	13455	0.97	4.0E-75	8922637	NT	CMO-NN0057-150400-335-a11 NN0057 Homo sapiens cDNA
987	6002	11033	2.28	3.0E-75	AF157623.1	NT	601303869F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5'
988	6002	11033	2.29	3.0E-75	AF157623.1	NT	Homo sapiens hypothetical protein FLJ10747 (FLJ10747), mRNA
1800	6791	11881	1.84	3.0E-75	AB011163.1	NT	Homo sapiens HTRA serine protease (PRSS1) gene, complete cds
1887	6878	11988	2.26	3.0E-75	5453871	NT	Homo sapiens HTRA serine protease (PRSS1) gene, complete cds
2053	7035	12147	0.82	3.0E-75	4507334	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFRL) mRNA
2356	7330	12446	3.59	3.0E-75	4759153	NT	Homo sapiens synaptobin 1 (SYNB1), mRNA
2855	7974	12989	0.8	3.0E-75	AL163201.2	NT	Homo sapiens synaptosomal-associated protein, 29kD (SNAP29) mRNA
3116	8132	13151	1.01	3.0E-75	AB011153.1	NT	Homo sapiens chromosome 21 segment HS21C001
3273	8285	13308	0.75	3.0E-75	M72393.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3273	8285	13309	0.75	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4044	9040	14031	1.58	3.0E-75	D87675.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4314	9308	14290	0.82	3.0E-75	7662421	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4998	9968		0.82	3.0E-75	AL163209.2	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
2239	7216	12334	30.85	1.0E-75	AW168135.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
2876	7895	12918	3.36	1.0E-75	X52221.1	NT	Homo sapiens chromosome 21 segment HS21C009
4552	9540	14525	1.71	1.0E-75	BE279301.1	EST_HUMAN	H.sapiens ERCC2 gene, exons 1 & 2 (partial)
4893	9965	14943	1.23	1.0E-76	BE894192.1	EST_HUMAN	601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'
45	5128	10116	3.62	9.0E-76	AB52648.1	EST_HUMAN	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'
45	5126	10117	3.62	9.0E-76	AB52648.1	EST_HUMAN	wb30b10.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235
							TRAP1;
							wb30b10.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235
							TRAP1;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
924	5941	10974	0.84	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
924	5941	10975	0.84	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
2839	7859	12879	1.17	8.0E-76	7706724	NT	Homo sapiens mediator (Sur2), mRNA
767	5788	10817	1.86	7.0E-76	5016092	NT	Homo sapiens dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
3220	8235	13256	3.47	7.0E-76	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
3228	8241	13263	7.12	7.0E-76	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
4246	9240	14223	4.97	7.0E-76	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
4246	9240	14224	4.97	7.0E-76	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
1214	6213		18.84	6.0E-76	BE398263.1	EST_HUMAN	601312019F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658757 5'
1903	6890	11983	15.24	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1903	6890	11984	15.24	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1903	6890	11985	15.24	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
3134	8150	13172	0.8	4.0E-76	BE814098.1	EST_HUMAN	QV3-BN0047-270700-283-g08 BN0047 Homo sapiens cDNA
623	5650	10653	1.54	3.0E-76	BF516262.1	EST_HUMAN	UIH-BW1-anz-b-04-0-JI.st NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
623	5650	10654	1.54	3.0E-76	BF516262.1	EST_HUMAN	UIH-BW1-anz-b-04-0-JI.st NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
1564	6561	11623	21.41	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1564	6561	11624	21.41	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3344	8353	13370	6.25	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
3344	8353	13371	6.25	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
278	5337	10351	1	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
340	5392	10398	1.94	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
340	5392	10399	1.94	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
458	5495		1.42	2.0E-76	4557662	NT	Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1) mRNA
565	5616	10615	1.68	2.0E-76	4503944	NT	Homo sapiens glucagon (GCG) mRNA
1014	6024	11058	1.16	2.0E-76	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1504	6502	11558	2.34	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1504	6502	11559	2.34	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
2768	7789	12811	3.35	2.0E-76	P23266	SWISSPROT	OLFATORY RECEPTOR-LIKE PROTEIN F5
3223	8238	13260	1.89	2.0E-76	AA445992.1	EST_HUMAN	zw64e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN
3223	8238	13261	1.89	2.0E-76	AA445992.1	EST_HUMAN	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR.1
3223	8238	13261	1.89	2.0E-76	AA445992.1	EST_HUMAN	zw64e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3398	8404	13430	1.04	2.0E-76	AB21149.1	EST_HUMAN	ac83b02.y6 Strategene lung (#937210) Homo sapiens cDNA clone IMAGE:869163 5' similar to TR:O14591 O14591 SIMILARITY TO P22059 ;
3682	8686	13888	7.33	2.0E-76	AA400700.1	EST_HUMAN	zr70g11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743398 5' similar to WP:R05D3.2 CE00281 ;
4400	9391	14375	1	2.0E-76	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4780	9774	14758	6.31	2.0E-76	AW878618.1	EST_HUMAN	QV3-OT0028-220300-132-b11 OT0028 Homo sapiens cDNA
4173	9168	14155	6.78	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
4173	9168	14156	6.78	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
187	6250	10281	3.03	8.0E-77	R83144.1	EST_HUMAN	yp11h02.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:187155 5' similar to SP-ANKB_HUMAN Q01484 ANKYRIN, BRAIN VARIANT 1 ;
4391	9382	14364	1.16	8.0E-77	BF205181.1	EST_HUMAN	SP-ANKB_HUMAN Q01484 ANKYRIN, BRAIN VARIANT 1 ;
1889	6378	11988	1.52	7.0E-77	AA625755.1	EST_HUMAN	zr91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
2345	7319	12439	9.62	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
2345	7319	12440	9.62	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
260	5319	10328	5.1	6.0E-77	4504600	NT	Homo sapiens Interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
1511	6509	11668	2.09	6.0E-77	AI204066.1	EST_HUMAN	qe77h12.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1745063 3'
4772	9756	14743	0.98	6.0E-77	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
4772	9756	14744	0.98	6.0E-77	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
1216	6215	11255	1.5	5.0E-77	AF041015.1	NT	7 Homo sapiens glucokinase (GCK) gene, exon 2
1343	6340	11391	2.76	5.0E-77	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2613	7575	12689	1.11	5.0E-77	AF162666.1	NT	Homo sapiens tousel-like kinase 1 (TLK1) mRNA, complete cds
2690	7848	12762	1.24	5.0E-77	4503160	NT	Homo sapiens cullin 1 (CUL1) mRNA
3443	8451	13476	1.75	5.0E-77	8394518	NT	Homo sapiens ubiquitin specific protease 18 (USP18), mRNA
4565	9553	14539	0.99	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
4565	9553	14540	0.99	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
4780	9764	14749	2.68	5.0E-77	AL043953.1	EST_HUMAN	DKFZp434G1728_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G1728 5'
3620	8627	13634	1.93	4.0E-77	AL449758.1	EST_HUMAN	AL449758 Homo sapiens fetal brain (Slavides GS) Homo sapiens cDNA
1928	6914	12010	1.57	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1928	6914	12011	1.57	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1334	6332	11380	2.09	2.0E-77	AV764617.1	EST_HUMAN	AV764617 MDS Homo sapiens cDNA clone MDSBTF10 5'
1407	6405	11464	7.17	2.0E-77	AW99712.1	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA
2045	7027	12138	5.42	2.0E-77	7706315	NT	Homo sapiens CGI-79 protein (LOC51634), mRNA
2518	7773	12602	2.22	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2518	7773	12603	2.22	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3922	8922	13913	1.53	2.0E-77	BE044316.1	EST_HUMAN	h043b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2_HUMAN P10264 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4288	9280	14268	0.82	2.0E-77	AI613519.1	EST_HUMAN	hw22g02.x1 NCL CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245
4288	9280	14269	0.82	2.0E-77	AI613519.1	EST_HUMAN	O65245 F21E10.7 PROTEIN ;
4465	9455		1.29	2.0E-77	4504068	NT	hw22g02.x1 NCL CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245
							O65245 F21E10.7 PROTEIN ;
							Homo sapiens glutamyl-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
4623	9608	14598	6.49	2.0E-77	AA653025.1	EST_HUMAN	ns66g12.s1 NCL CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1188838 similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L28. [1]; contains element MSR1 repetitive element ;
44	5124	10112	0.89	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
44	5124	10113	0.89	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
270	5329	10340	3.11	1.0E-77	4502169	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
270	5329	10341	3.11	1.0E-77	4502169	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
864	7733	10925	6.08	1.0E-77	4502169	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
864	7733	10926	6.08	1.0E-77	4502169	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1875	6884	11953	1.58	1.0E-77	AW059119.1	EST_HUMAN	hw63e05.x1 Soares_thymus_thymus_NHFTfH Homo sapiens cDNA clone IMAGE:2536160 3'
2376	7348	12469	1.33	1.0E-77	AB029024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
2971	7889	13002	2.25	1.0E-77	4503300	NT	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DECR1), mRNA
4227	9221	14201	4.08	1.0E-77	7706289	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
4393	9394	14366	17.29	1.0E-77	AJ229041.1	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
4516	9506	14488	2.27	1.0E-77	6552322	NT	q09g04.x1 NCL CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1981110 3'
4554	9542	14527	0.74	1.0E-77	AI273014.1	EST_HUMAN	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
4728	9713	14698	1.24	1.0E-77	11418424	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
4898	9877	14845	1.42	1.0E-77	7681849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
4898	9877	14846	1.42	1.0E-77	7681849	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
4989	9361	14341	0.68	1.0E-77	4758053	NT	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
84	5161	10172	2.28	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
84	5161	10173	2.28	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'

Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3240	8253	13274	0.88	6.0E-78	BF344101.1	EST_HUMAN	602016928F1 NCI_CGAP_Brt84 Homo sapiens cDNA clone IMAGE:4152511 5'
217	5280	10281	1.01	5.0E-78	11422488	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
2491	7459	12574	4.77	5.0E-78	AW673424.1	EST_HUMAN	ba54h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800405 5' similar to WP:Y48B6A.6
3301	8312	13339	4.18	5.0E-78	M5586.1	NT	CE22121 ;
1120	6126	11156	1.68	4.0E-78	AL043314.2	EST_HUMAN	Human collagenase type IV (CLG4) gene, exon 6
1487	6484	11539	1.28	4.0E-78	AL355841.1	NT	DKFZp434N0323_j1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
2254	7231	12350	20.59	4.0E-78	AF107405.1	NT	Novel human gene mapping to chromosome 22
4195	9188	14188	1.87	4.0E-78	7656878	NT	Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
4628	8613	14602	1.75	4.0E-78	4505806	NT	Homo sapiens synovial (LOC30816), mRNA
4628	8613	14603	1.75	4.0E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
160	5226	10235	3.27	3.0E-78	AF095901.1	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
160	5226	10236	3.27	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
2240	7217	12335	1.06	3.0E-78	4602142	NT	Homo sapiens eRF1 gene, complete cds
3142	8158	13180	1.34	3.0E-78	4507164	NT	Homo sapiens apoptosis inhibitor 3 (API3) mRNA
3678	8683		1.23	3.0E-78	AU140604.1	EST_HUMAN	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
3048	8065		2.47	2.0E-78	U04489.1	NT	AU140604 PLACE3 Homo sapiens cDNA clone PLACE3000373 5'
3907	8907		1.51	2.0E-78	AA311872.1	EST_HUMAN	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
5007	9978	14953	1.22	1.0E-78	4759843	NT	EST182583 Jurkat T-cells VI Homo sapiens cDNA 5' end
4660	9548	14533	3.65	9.0E-78	BE000837.1	EST_HUMAN	Homo sapiens nucleoporin 155KD (NUP155) mRNA
4714	9639	14684	5.64	9.0E-78	AL163210.2	NT	Homo sapiens peptide YY (PYY), mRNA
3657	8663	13668	0.91	8.0E-78	D28476.1	NT	RC2-BN0074-030300-014-c12 BN0074 Homo sapiens cDNA
4366	8357	14337	1.57	8.0E-78	D28476.1	NT	Homo sapiens chromosome 21 segment HS21C010
4366	8357	14338	1.57	8.0E-78	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
3179	8195	13218	19.1	7.0E-78	BE618648.1	EST_HUMAN	Human mRNA for KIAA0045 gene, complete cds
3103	8119		0.99	4.0E-78	8822325	NT	601472766T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875657 3'
311	5366	10377	1.61	3.0E-78	AF114488.1	NT	Homo sapiens hypothetical protein FLJ10283 (FLJ10283), mRNA
863	5978	11012	5.56	3.0E-78	AF232708.1	NT	Homo sapiens intercalin short isoform (ITSN) mRNA, complete cds
3025	8042	13061	2.52	3.0E-78	U09410.1	NT	Homo sapiens cell-line tsA201a chloride ion current inducer protein I(Cin) gene, complete cds
285	5343		1.02	2.0E-78	H63129.1	EST_HUMAN	Human zinc finger protein ZNF131 mRNA, partial cds
628	5658	10661	1.22	2.0E-78	BE379926.1	EST_HUMAN	ly48f03.s1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:208541 3'
815	5931	10966	1.47	2.0E-78	4757841	NT	601159415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511107 5'
1018	6028		1.19	2.0E-78	AI52347.1	EST_HUMAN	Homo sapiens BCL2-like 2 (BCL2L2) mRNA
1751	6745	11824	0.92	2.0E-78	7657024	NT	ht18h07.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2118685 3'
							Homo sapiens Dickkopf gene 4 (DKK-4), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1751	6745	11825	0.92	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA
2087	7068	12180	3.3	2.0E-79	4555863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2087	7068	12181	3.3	2.0E-79	4555863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2130	7110	12223	2.05	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
2249	7226	12346	2.65	2.0E-79	AF244138.1	NT	Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds
4041	9037	14027	1.34	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
3073	8089	13102	18.41	9.0E-80	AA725848.1	EST_HUMAN	al236d05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
3073	8089	13103	18.41	9.0E-80	AA725848.1	EST_HUMAN	al236d05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
3521	8528		1.06	8.0E-80	U94387.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
4797	9781	14764	1.67	7.0E-80	H04619.1	EST_HUMAN	y49d02.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152087 5'
889	5907	10947	2.22	6.0E-80	AI422197.1	EST_HUMAN	ff58d02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW.NUEM_HUMAN
1604	6600	11661	2.05	6.0E-80	U64898.1	NT	Q16785 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;
2234	7211	12327	4.78	6.0E-80	6631094	NT	Homo sapiens NRD convertase mRNA, complete cds
2234	7211	12328	4.78	6.0E-80	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
4182	9157	14142	1.33	6.0E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
4162	9157	14143	1.33	6.0E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
583	5614	10614	5.48	5.0E-80	4506228	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA
825	5845	10882	1.83	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MN1H) mRNA, complete cds
825	5845	10883	1.83	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MN1H) mRNA, complete cds
1169	6172		1.23	5.0E-80	X91647.1	NT	H. sapiens nci1 gene (exon 12)
1429	6426		1.63	5.0E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2300	7276	12394	1.18	6.0E-80	U89358.1	NT	Human J(3)mbt protein homolog mRNA, complete cds
2363	7337	12454	8.73	6.0E-80	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
2722	7678	12782	6.29	5.0E-80	4504292	NT	Homo sapiens H3 histone family, member J (H3F-J) mRNA
4796	9780	14783	1.24	5.0E-80	AL163298.2	NT	Homo sapiens chromosome 21 segment HS21C063
216	5279		15.21	3.0E-80	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4571	9559	14548	1.41	3.0E-80	BF085009.1	EST_HUMAN	PMO-GN0018-040900-002-E03 GN0018 Homo sapiens cDNA
4753	9738		7.56	3.0E-80	BE817465.1	EST_HUMAN	QV4-BN0263-040600-241-g10 BN0263 Homo sapiens cDNA
1762	6754	11839	3.95	2.0E-80	R35321.1	EST_HUMAN	y65608.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:38060 5'
1823	6813	11907	1.48	2.0E-80	AI444821.1	EST_HUMAN	RET487 subtracted retina cDNA library Homo sapiens cDNA clone RET487
2002	6985	12089	3.58	2.0E-80	AL043116.2	EST_HUMAN	DKFzP434D1323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFzP434D1323 5'

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
338	5390		1.79	1.0E-80	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
791	5812	10842	1.53	1.0E-80	AF231920.1	NT	Homo sapiens chromosome 21-unknown mRNA
1914	6900		2.27	1.0E-80	AI732656.1	EST_HUMAN	nm01112.x6 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1076495 3' similar to contains OFR.11 OFR repetitive element ;
4874	9659	14642	0.85	1.0E-80	N99520.1	EST_HUMAN	z339g07.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294972 5' similar to contains Alu repetitive element;
2144	7123	12239					ze21d10.1 Scores_fetal_heart_NbhH19W Homo sapiens cDNA clone IMAGE:359635 5' similar to SW:KRHA_RABIT Q02957 KERATIN, GLYCINE/TYROSINE-RICH OF HAIR. [1]; contains element MER22 repetitive element ;
4262	9255	14244	0.95	7.0E-81	AA011080.1	EST_HUMAN	
4262	9255	14244	6.63	6.0E-81	BE256829.1	EST_HUMAN	
2155	7134	12253	5.16	5.0E-81	BE268042.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5' 601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5' 6011125509F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345480 5'
1786	6778	11870	1.6	4.0E-81	AW779612.1	EST_HUMAN	hm98d02.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3035907 3' similar to SW:COFG_BOVIN P53620 COATOMER GAMMA SUBUNIT ;
3097	8113	13131	3.69	4.0E-81	AB037768.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds ws90h03.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:2505269 3' similar to TR:O43815 O43815 STRATIN. ;
3544	8551	13558	0.78	4.0E-81	AW004608.1	EST_HUMAN	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4036	9032	14019	2.04	4.0E-81	AF263308.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4036	9032	14020	2.04	4.0E-81	AF263308.1	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
4268	9261	14251	0.99	4.0E-81	8923209	NT	
1248	6246	11285	12.27	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
1248	6246	11286	12.27	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2310	7285	12405	1.5	3.0E-81	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
2922	7941	12957	5.68	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2922	7941	12958	5.68	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2759	7780	12804	2.23	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
2759	7780	12805	2.23	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
3686	8690	13693	0.83	2.0E-81	AW611542.1	EST_HUMAN	hg56c01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2852384 3'
3688	8575	13581	1.35	1.0E-81	AW606558.1	EST_HUMAN	EST372729 IMAGE resequences, MAGF Homo sapiens cDNA
4384	9375	14354	2.11	1.0E-81	AA040370.1	EST_HUMAN	zk45h09.1 Scores_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:485825 5' similar to PIR:S52437 S52437 CDP-diacylglycerol synthase - fruit fly ;
4510	9500	14479	10.97	1.0E-81	BE047986.1	EST_HUMAN	tz45c04.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291528 5'

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13	5093	10077	4.69	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
107	5093	10077	5.26	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
261	5320	10330	2.65	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
804	5825	10855	2.38	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
876	5894	10935	1.93	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
1459	6456	11516	1.39	8.0E-82	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1817	6614	11681	1.23	8.0E-82	671660.1	NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
4121	8115	14102	0.84	8.0E-82	8923432	NT	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA
1424	8421	12765	1.04	7.0E-82	BF035327.1	EST_HUMAN	601468531F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3852086 5'
2693	7651	12765	1.55	7.0E-82	AU144050.1	EST_HUMAN	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000762 3'
1632	6829	11698	100.34	4.0E-82	AF081484.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
278	5334	10347	16.31	3.0E-82	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
693	5717	10734	3.55	3.0E-82	BE005705.1	EST_HUMAN	RC2-BN0120-010400-013-02 BN0120 Homo sapiens cDNA
778	5800	10830	5.3	3.0E-82	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
859	5878	10919	8.88	3.0E-82	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1044	6054	10822	80.59	3.0E-82	AA25848.1	EST_HUMAN	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
1337	6335	11365	0.96	3.0E-82	AW875073.1	EST_HUMAN	RC6-PT0001-190100-021-B02 PT0001 Homo sapiens cDNA
1438	6435	11492	2.02	3.0E-82	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1860	6849	11837	1.68	3.0E-82	BE813232.1	EST_HUMAN	RC1-BN0005-260700-018-g04 BN0005 Homo sapiens cDNA
3198	8214	10621	2.15	3.0E-82	545381.1	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA
592	5823	10621	1.39	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
592	5823	10622	1.39	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1647	6643	11715	1.78	2.0E-82	AL046390.1	EST_HUMAN	DKFZp434M117.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434M117 5'
3756	8759	13758	0.85	2.0E-82	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4112	9108	14092	0.83	2.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4426	9416	14403	1.06	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1098 protein, partial cds
4426	9416	14404	1.08	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1098 protein, partial cds
4720	9705	14691	2.77	2.0E-82	AF045555.1	NT	Homo sapiens wbscr1 (WBSCR1) and wbscr5 (WBSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
4908	9887	14859	1.58	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
4908	9887	14860	1.58	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
587	5618	10616	1.67	1.0E-82	11545921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
1189	6190		1.57	1.0E-82	BE885106.1	EST_HUMAN	601510859F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912207 5'
1268	6264	11305	3.2	1.0E-82	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
1267	6265	11308	1.14	1.0E-82	AB011110.2	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
1389	6386	11438	4.62	8.0E-83	BE383973.1	EST_HUMAN	601273346F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614382 5'
1842	7700	11709	4.3	8.0E-83	N86951.1	EST_HUMAN	z448f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
1339	6337	11386	1.87	7.0E-83	AW385528.1	EST_HUMAN	QV4-LT0016-271299-068-h11 LT0016 Homo sapiens cDNA
2784	7814		1.62	7.0E-83	AA584655.1	EST_HUMAN	nc12h01.s1 NCI_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element;
4670	9655		6.92	7.0E-83	BF221813.1	EST_HUMAN	7p37a07.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:3647893 3' similar to TR:Q9Y316 Q9Y316 DJ207H1.1;
5036	10007		1.51	7.0E-83	BF221813.1	EST_HUMAN	7p37a07.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:3647893 3' similar to TR:Q9Y316 Q9Y316 DJ207H1.1;
401	5437	10458	1.97	6.0E-83	M33320.1	NT	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
1749	6743	11822	7.97	6.0E-83	AW573088.1	EST_HUMAN	h31h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833525 3' similar to
2977	7895		1.02	6.0E-83	AF231919.1	NT	SW:YBEB_HAEIN P44471 HYPOTHETICAL PROTEIN H10034.;
2996	8014	13026	1.01	6.0E-83	AA701457.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
3483	8491	13507	0.82	6.0E-83	U17883.1	NT	z159c05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435080 3'
832	5949		1.95	5.0E-83	U17883.1	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1897	7704		2.85	5.0E-83	AF006305.1	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5
3553	8560	13566	1.13	5.0E-83	AL133207.2	NT	Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds
3810	8813	13819	0.99	5.0E-83	4885180	NT	Novel human gene mapping to chromosome X
4907	9886	14857	14.02	5.0E-83	4557013	NT	Homo sapiens deoxyribonuclease I (DNASE1), mRNA
4907	9886	14858	14.02	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
634	5682	10667	1.76	4.0E-83	AF224669.1	NT	Homo sapiens catalase (CAT) mRNA
3435	8443	13469	1.08	4.0E-83	BE880078.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
982	5997		3.78	3.0E-83	AA368311.1	EST_HUMAN	601511580F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913195 5'
2705	7682		1.44	3.0E-83	AA632854.1	EST_HUMAN	EST79542 Placenta 1 Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9
1764	6756	11841	1.7	2.0E-83	AA893492.1	EST_HUMAN	np87c07.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133292 similar to contains THR.12 THR repetitive element;
							ct84g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1821592 3' similar to TR:Q92614 Q92614 MYELOBLAST KIAA0218.;

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1764	6756	11842	1.7	2.0E-83	AA993492.1	EST_HUMAN	084g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q82614
1884	6873	11862	3.01	2.0E-83	N66951.1	EST_HUMAN	Q82614 MYELOBLAST KIAA0216 ;
2779	7800	12818	2.73	2.0E-83	BE82694.1	EST_HUMAN	2948f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
3185	8211		2.22	2.0E-83	11430834	NT	RC8-ET0048-280600-013-H12 ET0048 Homo sapiens cDNA
3697	8691		0.74	2.0E-83	AL163202.2	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
4210	9203	14185	4.16	2.0E-83	AF202879.1	NT	Homo sapiens chromosome 21 segment HS21C002
4517	9507	14487	6.32	2.0E-83	7706398	NT	Homo sapiens hematopoietic progenitor cell antigen CD34 precursor (CD34) mRNA, partial cds
4517	9507	14488	6.32	2.0E-83	7706398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
1387	6384	11435	2.31	1.0E-83	4504326	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
1387	6384	11436	2.31	1.0E-83	4504326	NT	Homo sapiens hydroxyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
2585	7548	12693	1.22	1.0E-83	BE863690.1	EST_HUMAN	Homo sapiens hydroxyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
3777	8780	13783	5.31	1.0E-83	AF053768.1	NT	601507376F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3908754 5'
4122	8116	14103	3.74	1.0E-83	Z25822.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP80 mRNA, partial cds
4733	9718	14703	2.36	1.0E-83	4502166	NT	H. sapiens gene for mitochondrial dodecanoyl-CoA delta-isomerase, exon 3
3707	8711	13714	4.14	7.0E-84	BE801209.1	EST_HUMAN	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1276	6274	11313	2.87	6.0E-84	BE838664.1	EST_HUMAN	601676023F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3958853 5'
1276	6274	11314	2.87	6.0E-84	BE838664.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
2334	7308	12429	3.11	6.0E-84	AA776574.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
5044	10015	14994	0.98	6.0E-84	R05859.1	EST_HUMAN	aa86a03.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3'
704	6728	10745	0.8	5.0E-84	AA382811.1	EST_HUMAN	ye83a04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125262 5'
2945	7984		1.24	5.0E-84	AF109718.1	NT	EST96094 Testis 1 Homo sapiens cDNA 5' end
1386	6383	11434	2.71	4.0E-84	AI695321.1	EST_HUMAN	Homo sapiens chromosome 3 subtelomeric region
4782	9776	14760	1.93	4.0E-84	4505928	NT	wa76c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to SW:NRDC_HUMAN O43847 NARDILYSIN PRECURSOR ;
4783	9777	14761	1.73	4.0E-84	AF069601.2	NT	Homo sapiens polymerase (DNA-directed), alpha (70kD) (POLA2), mRNA
314	6369	10380	1.77	3.0E-84	AF026200.1	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
1920	6906	12000	1.89	3.0E-84	5453855	NT	Homo sapiens Bach1 protein homolog mRNA, partial cds
1958	6944	12048	3.98	3.0E-84	AL096880.1	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
3510	8518	13529	0.97	3.0E-84	AB026898.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3662	8667	13873	5.61	3.0E-84	AF014459.1	NT	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLR51) mRNA, complete cds
2047	7028	12141	4.68	2.0E-84	BE95397.1	EST_HUMAN	CM1-BT0785-190600-272-b08 BT0785 Homo sapiens cDNA
2047	7028	12142	4.68	2.0E-84	BE95397.1	EST_HUMAN	CM1-BT0785-190600-272-b08 BT0785 Homo sapiens cDNA
2873	7892	12915	8.93	2.0E-84	AF036943.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
2892	7911	12932	1.41	2.0E-84	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
310	5365	10376	1.21	1.0E-84	AF114488.1	NT	Homo sapiens interseitin short isoform (ITSN) mRNA, complete cds
545	5579	10583	16.86	1.0E-84	4507852	NT	Homo sapiens tyrosine 3-monooxygenase/tyrosine 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA
710	6734	11427631	1.23	1.0E-84	11427631	NT	Homo sapiens complement component 5 (C5), mRNA
1274	6272	11311	2.76	1.0E-84	AA984379.1	EST_HUMAN	am85b11.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629885 3'
2001	6984	12088	1.8	1.0E-84	BE392137.1	EST_HUMAN	601308006f1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626257 5'
2162	7141	12258	1.8	1.0E-84	11427197	NT	Homo sapiens pericentriolar material 1 (PCM1), mRNA
3665	8670	13875	2.55	1.0E-84	AA720851.1	EST_HUMAN	hw12e06.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239108 3'
4282	9284	14271	4.33	1.0E-84	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4581	9549	14534	2.83	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
4581	9549	14535	2.93	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
4756	9284	14271	2.67	1.0E-84	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4952	9929	14907	0.71	1.0E-84	AW371947.1	EST_HUMAN	RC4-BT0311-141299-012-g06 BT0311 Homo sapiens cDNA
4952	9929	14908	0.71	1.0E-84	AW371947.1	EST_HUMAN	RC4-BT0311-141299-012-g06 BT0311 Homo sapiens cDNA
952	5968	11094	2.75	9.0E-85	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1056	6065	11094	10.8	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1056	6065	11095	10.8	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1543	6541	11598	1.1	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1543	6541	11599	1.1	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1635	6632	11702	2.05	9.0E-85	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
3711	8715	13717	0.81	9.0E-85	7019418	NT	Homo sapiens nucleolar GTPase (HUMAUNTIQ), mRNA
4130	9126	14109	1.08	9.0E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4638	9624	14615	1.44	9.0E-85	M33764.1	NT	Human ornithine decarboxylase gene, complete cds
4639	9624	14616	1.44	9.0E-85	M33764.1	NT	Human ornithine decarboxylase gene, complete cds
4757	9741	14726	1.1	9.0E-85	AL163286.2	NT	Homo sapiens chromosome 21 segment HS21C068
1119	6125	11155	34.29	7.0E-85	LO5094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
2271	7247	12364	2.11	5.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1280	6278	11320	0.77	3.0E-85	AF090157.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6
1742	6737	11813	6.32	3.0E-85	T97495.1	EST_HUMAN	yec3g09.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:121504 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4188	9181	14184	1.26	3.0E-85	BE287189.1	EST_HUMAN	601189704F2 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3533616 5'
4743	9728	14714	1.48	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4743	9728	14715	1.48	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4809	9793	14775	1	3.0E-85	7363442	NT	Homo sapiens olfactory receptor, family 12, subfamily D, member 2 (OR12D2), mRNA
948	5984	10988	0.72	2.0E-85	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1023	6033	11084	1.98	2.0E-85	AF248540.1	NT	Homo sapiens Intersectin 2 (SH3D1B), mRNA, complete cds
1380	6377	11425	1.33	2.0E-85	7706205	NT	Homo sapiens CGI-201 protein (LOC51340), mRNA
1395	6392	11445	7.52	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2), mRNA
1395	6392	11446	7.52	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2), mRNA
2169	7148	12265	1.4	2.0E-85	U10525.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2750	6315	12990	10.24	2.0E-85	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2958	7875	12990	2.18	2.0E-85	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4207	9200	14182	5.76	2.0E-85	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4755	9740	14725	0.97	2.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2223	7200	12423	3.19	1.0E-85	BE794306.1	EST_HUMAN	601591416F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945818 5'
2328	7303	12423	5.67	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866021 5'
2329	7303	12424	5.67	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866021 5'
1404	6401	10972	54.78	9.0E-86	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2987690 5'
923	5940	10972	0.75	7.0E-86	AA860801.1	EST_HUMAN	aj88f08.s1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
923	5940	10973	0.75	7.0E-86	AA860801.1	EST_HUMAN	aj88f08.s1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
1275	6273	11312	2.27	6.0E-86	4505492	NT	Homo sapiens oxoglutarate dehydrogenase (lipoamide) (OGDH), mRNA
5001	9972	14948	1.8	6.0E-86	6005833	NT	Homo sapiens 24 kDa intrinsic membrane protein (PMP24), mRNA
211	5274	10288	1.35	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
284	5323	10332	2.04	2.0E-86	AA306264.1	EST_HUMAN	EST177232 Jurkat T-cells VI Homo sapiens cDNA 5' end
411	5448	11207	2.83	2.0E-86	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2128	7108	12222	1.94	2.0E-86	N58977.1	EST_HUMAN	aj219a08.r1 Soares multiple sclerosis_2NbHMSF Homo sapiens cDNA clone IMAGE:283478 5'
2207	7184	12307	3.37	2.0E-86	AB033103.1	NT	Human endogenous retrovirus, complete genome
3331	8341	13359	1.08	2.0E-86	AB033103.1	NT	Homo sapiens mRNA for KIAA1277 protein, partial cds
3681	8666	13671	1.19	2.0E-86	AW966142.1	EST_HUMAN	EST378215 MAGE resequences, MAGI Homo sapiens cDNA
3681	8666	13671	2.84	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3681	8666	13672	2.84	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3927	8927	14625	2.69	2.0E-86	AW515742.1	EST_HUMAN	hd87g08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2816542 3'
4845	9630	14825	3.42	2.0E-86	AF058490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1562	6559	11621	2.08	1.0E-88	4826855	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1) mRNA
3089	8105	13120	1.45	1.0E-86	5453649	NT	Homo sapiens fibulin 5 (FBLN5) mRNA
3164	8180	13202	2.88	1.0E-86	L20482.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
3222	8237	13258	1.17	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3222	8237	13259	1.17	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3842	8844	13852	1.22	1.0E-86	7706161	NT	Homo sapiens hypothetical protein (LOC513118), mRNA
3842	8844	13853	1.22	1.0E-86	7706161	NT	Homo sapiens hypothetical protein (LOC513118), mRNA
4142	9137	14121	5.37	1.0E-86	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
476	5512	10525	131.14	8.0E-87	X62245.1	NT	O. cuniculus mRNA for elongation factor-1 alpha
2233	7210	12325	1.99	7.0E-87	BF063211.1	EST_HUMAN	7n85102.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:3322779 3'
2233	7210	12326	1.99	7.0E-87	BF063211.1	EST_HUMAN	7n85102.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:3322779 3'
3448	8456	13482	0.78	6.0E-87	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
1140	6145	11176	2.38	5.0E-87	AA382811.1	EST_HUMAN	EST196094. Testis 1 Homo sapiens cDNA 5' end
951	5967	11000	1.12	4.0E-87	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1153	6157	11190	18.02	4.0E-87	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1980	6965	12071	1.85	4.0E-87	AB007925.1	NT	Homo sapiens mRNA for KIAA0456 protein, partial cds
2355	7328	12444	1.2	4.0E-87	7706299	NT	Homo sapiens CGI-60 protein (LOC51826), mRNA
2355	7328	12445	1.2	4.0E-87	7706299	NT	Homo sapiens CGI-60 protein (LOC51826), mRNA
3383	8391	13414	1.88	4.0E-87	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2704	7661	12773	5.54	2.0E-87	4885420	NT	Homo sapiens high-mobility group (nonhistone chromosome) protein 4 (HMG4) mRNA
2878	7897		1.17	2.0E-87	BF327920.1	EST_HUMAN	QV0-BN0148-050600-254-a03 BN0148 Homo sapiens cDNA
3696	8700	13703	0.88	2.0E-87	AU116935.1	EST_HUMAN	AU116935 HEMBA1 Homo sapiens cDNA clone HEMBA1000307 5'
4758	9742	14727	0.66	2.0E-87	BF376311.1	EST_HUMAN	CMO-TN0038-150900-552-h08 TN0038 Homo sapiens cDNA
1163	7698		1.89	1.0E-87	7705683	NT	Homo sapiens putative glycolipid transfer protein (LOC51034), mRNA
1406	6403	11460	1.69	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141089-001-g04 CT0265 Homo sapiens cDNA
1406	6403	11461	1.69	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141089-001-g04 CT0265 Homo sapiens cDNA
3628	8635	13640	13.27	1.0E-87	Y00052.1	NT	Homo sapiens mRNA for T-cell cyclophilin
3849	8655	13661	2.3	1.0E-87	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
809	5926	10861	0.7	9.0E-88	5453887	NT	Homo sapiens protease inhibitor 4 (kallistatin) (PI4) mRNA
1089	6096	11125	6.3	9.0E-88	AF167465.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1331	6329	11377	2.48	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
1331	6329	11378	2.48	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3542	8548	13557	0.89	9.0E-88	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4147	9142	14126	3.04	9.0E-88	X91929.1	NT	H. sapiens ECE-1 gene (exon 9)
4147	9142	14127	3.04	9.0E-88	X91929.1	NT	H. sapiens ECE-1 gene (exon 8)
1792	6783		1.98	5.0E-88	7661887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
2568	7531	12650	4.82	5.0E-88	N89399.1	EST_HUMAN	K9710F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
2831	7850	12867	0.71	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
2941	7980	12979	0.76	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
2941	7980	12980	0.76	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
3305	8316		2.56	5.0E-88	AI693217.1	EST_HUMAN	wd88h08.x1 NC1 CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2336789 3' similar to contains Alu repetitive element; contains element MER22 MER23 repetitive element;
3458	8468	13493	0.7	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
1309	6307	11355	1.13	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
1309	6307	11356	1.13	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
722	5745	10784	1.4	3.0E-88	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
1776	6768		2.26	3.0E-88	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
2877	7896	12820	4.85	3.0E-88	N66951.1	EST_HUMAN	z948f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
4118	9112	14096	0.69	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase (domain 23 (ADAM23) mRNA
4118	9112	14097	0.69	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase (domain 23 (ADAM23) mRNA
4351	9342		3.64	3.0E-88	11428300	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
1019	6029	11058	1.27	2.0E-88	7305198	NT	Homo sapiens Caldesin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1585	6582	11644	1.92	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1711	6706	11782	4.8	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3384	8392	13415	0.99	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4301	9293	14280	2.35	2.0E-88	5031666	NT	Homo sapiens dynamin, exophenol, light polypeptide 4 (DNAL4), mRNA
2861	7620	12732	1.49	8.0E-89	BE311557.1	EST_HUMAN	601142409F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506186 5'
430	5488	10486	1.24	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
430	5488	10487	1.24	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
4730	9715	14700	3.49	7.0E-89	4557380	NT	Homo sapiens complement component 8, beta polypeptide (C8B) mRNA
4774	9759	14746	5.7	7.0E-89	AL045748.1	EST_HUMAN	DKFZp434E246_r1 434 (synonym: hless3) Homo sapiens cDNA clone DKFZp434E246 5'
1007	6017	11047	2.12	6.0E-89	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
2161	7130	12247	1.98	6.0E-89	4506124	NT	Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4) mRNA
2368	7340	12456	5.05	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
2368	7340	12457	5.05	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3446	8454	13480	0.75	6.0E-89	7661817	NT	Homo sapiens HSPC159 protein (HSPC159), mRNA
4354	8345	14324	0.81	6.0E-89	7661737	NT	Homo sapiens HSPC019 protein (HSPC019), mRNA
4503	8493	14470	3.9	6.0E-89	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4503	8493	14471	3.9	6.0E-89	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4903	9882	14852	3.31	6.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
4903	9882	14853	3.31	6.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
2807	7827	12843	0.95	3.0E-89	AW976181.1	EST_HUMAN	EST388290 MAGI resequences, MAGN Homo sapiens cDNA
127	5442	10462	0.87	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
127	5442	10463	0.87	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
526	5561	10584	0.68	2.0E-89	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
2611	7831	12847	1.44	2.0E-89	A1222095.1	EST_HUMAN	q99608.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb.J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN)/contains Alu repetitive element
4022	8018	14005	1.18	2.0E-89	AF089897.1	NT	Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds
4030	9026	14014	4.76	2.0E-89	X58742.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4030	9026	14015	4.76	2.0E-89	X58742.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4223	9217	14186	1.09	2.0E-89	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4367	9359	14339	1.05	2.0E-89	AJ007378.1	NT	Homo sapiens GGT gene, exon 5
1046	6056	11084	3.19	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1047	6056	11084	2.72	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1310	7744	11357	3.68	8.0E-90	BE870561.1	EST_HUMAN	7636108.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
1310	7744	11358	3.68	8.0E-90	BE870561.1	EST_HUMAN	7636108.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
826	5846		4.22	7.0E-90	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2894	8012	13024	1.08	6.0E-90	X91926.1	NT	H.sapiens ECE-1 gene (exon 6)
2894	8012	13025	1.08	6.0E-90	X91926.1	NT	H.sapiens ECE-1 gene (exon 6)
4105	8089	14085	9.58	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4105	8089	14086	9.58	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
154	5220		78.69	5.0E-90	AB035344.1	NT	Homo sapiens TOL6 gene, exon 1-10b
1173	6176	11210	2.39	5.0E-90	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds

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1784	6776	11867	1.48	5.0E-90	A1222095.1	EST_HUMAN	q996c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL-TRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;
1784	6776	11868	1.48	5.0E-90	A1222095.1	EST_HUMAN	q996c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL-TRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;
2484	7452	12566	1.82	5.0E-90	AF114487.1	NT	Homo sapiens Intersectin long isoform (ITSN) mRNA, complete cds
300	5357	10369	2.4	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
300	5357	10370	2.4	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1070	6078	11109	3.28	4.0E-90	4505316	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1650	6846	11719	9.18	4.0E-90	X99033.1	NT	H sapiens gene encoding discoidin receptor tyrosine kinase, exon 16
4522	9512	14497	4.85	4.0E-90	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4653	8638	14629	1.95	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4873	9658	14641	1.82	4.0E-90	M85667.1	NT	Human prothormone converting enzyme (NEC2) gene, exon 8
5010	9981	14956	0.92	4.0E-90	5729777	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
213	5276	10290	4.2	2.0E-90	BE537813.1	EST_HUMAN	601067378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834 5'
1154	6158	11191	71.49	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1154	6158	11192	71.49	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
3755	8758	13757	1.88	2.0E-90	A1138213.1	EST_HUMAN	q54c02.x1 Soares_placenta_8to9weeks_2NbhP8pc9W Homo sapiens cDNA clone IMAGE:1713410 3'
4550	9538	14524	0.97	2.0E-90	AB006627.1	NT	similar to SW-OLF3_MOUSE P23275 OLFACTORY RECEPTOR OR3. ;
4754	9739	14724	8.45	2.0E-90	5728855	NT	Homo sapiens mRNA for KIAA0289 gene, partial cds
							Homo sapiens GRB2-related adaptor protein (GRAP) mRNA
274	5333	10346	5.3	1.0E-90	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
373	7693	10436	1.98	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
374	7693	10436	1.9	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
686	5710	10723	1.73	1.0E-90	AJ237569.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
686	5710	10724	1.73	1.0E-90	AJ237569.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
720	5743	10761	11.11	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
720	5743	10762	11.11	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1093	6100		3	1.0E-90	4507828	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1287	6286	11329	2.29	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1287	6286	11330	2.29	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1628	6625		4.57	1.0E-90	BE379884.1	EST_HUMAN	601169563F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:351118 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1861	6850	11938	2.56	1.0E-90	11420514	NT	Homo sapiens similar to SALL1 (sal (Drosophila)-like (LOC57167), mRNA
2760	7801	12819	9.3	1.0E-90	6005720	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
3761	8764	13765	0.99	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0803 protein, partial cds
3761	8764	13766	0.99	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0803 protein, partial cds
4289	9291	14278	1.62	1.0E-90	AF167340.1	NT	Homo sapiens soluble Interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced
4073	9087	14057	6.87	8.0E-91	AD12234.1	EST_HUMAN	HUM0003381 Liver HepG2 cell line. Homo sapiens cDNA clone s381 3'
3394	8402	13428	2.26	5.0E-91	AA702794.1	EST_HUMAN	z80b04.s1 Soares_fetal_liver_spleen_1NFLS_ST Homo sapiens cDNA clone IMAGE:448015 3'
4385	9376	14355	1.19	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y78AA1 Homo sapiens cDNA clone Y78AA1002087 5'
4385	9376	14358	1.19	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y78AA1 Homo sapiens cDNA clone Y78AA1002087 5'
4684	9649	14636	1.09	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
4664	9649	14637	1.09	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
3129	8145	13165	1.87	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3129	8145	13166	1.87	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
1578	6575	11637	1.86	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1578	6575	11638	1.86	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1754	7701	11830	1.4	3.0E-91	AF265555.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
3265	8278	13301	1.55	3.0E-91	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3380	8388	13410	3.62	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3380	8388	13411	3.62	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3699	8703	13708	1.57	3.0E-91	AF084530.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
4458	9448	14428	6.17	3.0E-91	U30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4820	9804	14785	1.2	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4820	9804	14786	1.2	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
49	5130	10124	2.61	1.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1226	6225	11271	5.11	1.0E-91	AW449746.1	EST_HUMAN	UI-H-B13-aks-d-01-0-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735280 3'
1222	6222	11265	7.33	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
1222	6222	11266	7.33	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
283	5168	10178	6.58	8.0E-92	W26397.1	EST_HUMAN	2663 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
25	5105	10354	7.99	8.0E-92	BE386363.1	EST_HUMAN	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
235	7716	10307	2.65	7.0E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
235	7716	10308	1	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
586	5617		0.93	7.0E-92	AF007822.1	NT	Homo sapiens cytoplasmic Seprase truncated isoform mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1261	6269	11302	2.83	7.0E-92	4502384	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2123	7103	12215	8.39	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2123	7103	12216	8.39	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2493	7461	12576	2.56	7.0E-92	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2653	7613	12723	5.83	7.0E-92	6005738	NT	Homo sapiens NRAS-related gene (DYS155E), mRNA
2679	7637	12752	0.93	7.0E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
3270	10047	13304	0.67	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3270	10047	13305	0.67	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4455	9445	14425	1.24	7.0E-92	S71824.1	NT	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
4455	9445	14426	1.24	7.0E-92	S71824.1	NT	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
4844	9828	14801	0.94	7.0E-92	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
1552	6549		1.37	5.0E-92	BE390382.1	EST_HUMAN	601283012F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605018 5'
2692	7650	12764	2.21	3.0E-92	BE909714.1	EST_HUMAN	601501242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902939 5'
26	5108	10090	1.42	2.0E-92	4501898	NT	Homo sapiens activin A receptor, type IIB (ACVR2B) mRNA
178	5241	10251	3.37	2.0E-92	11422946	NT	Homo sapiens hypothetical protein dJ462023.2 (DJ462023.2), mRNA
178	5241	10252	3.37	2.0E-92	11422946	NT	Homo sapiens hypothetical protein dJ462023.2 (DJ462023.2), mRNA
740	5763	10787	2.34	2.0E-92	BE289180.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
740	5763	10788	2.34	2.0E-92	BE289180.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
1676	6672		1.45	2.0E-92	S78653.1	NT	mrg=mas-related [human, Genomic, 2416 nt]
1896	6884	11976	1.59	2.0E-92	A1818119.1	EST_HUMAN	wk27d07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
1896	6884	11977	1.59	2.0E-92	A1818119.1	EST_HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
1985	6978	12094	8.59	2.0E-92	4506860	NT	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
2888	7551	12888	15.93	2.0E-92	6912457	NT	Homo sapiens syndecan 4 (amphiglycan, rylodcan) (SDC4) mRNA
2756	6811	11676	3.69	2.0E-92	11418424	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2756	6811	11677	3.69	2.0E-92	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
3532	8538	13543	1.16	2.0E-92	AF231919.1	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
3532	8538	13544	1.16	2.0E-92	AF231919.1	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
3602	8609	13617	5.87	2.0E-92	5803180	NT	Homo sapiens chromosome 21 unknown mRNA
4165	9160	14147	1.16	2.0E-92	M10976.1	NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA
							Human endogenous retroviral DNA (4-1), complete proviral segment

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4835	9819		2.79	2.0E-92	AL040437.1	EST_HUMAN	DKFZp434C0414_r1_434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434C0414 5'
1813	6803	11895	2.03	1.0E-92	R78078.1	EST_HUMAN	y80e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
1813	6803	11898	2.03	1.0E-92	R78078.1	EST_HUMAN	y80e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
2020	7003	12108	40.93	1.0E-92	4506668	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA
1879	6864	12070	2.63	9.0E-93	AU121681.1	EST_HUMAN	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
1991	6978		27.81	9.0E-93	AA318723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
3534	8540	13546	1.75	9.0E-93	BE388871.1	EST_HUMAN	601281867F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603832 5'
4208	9202	14184	1.1	9.0E-93	AU121681.1	EST_HUMAN	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
244	5304	10314	8.34	7.0E-93	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1362	6359	11409	2.07	5.0E-93	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
1363	6380	11428	8.53	5.0E-93	AB74184.1	EST_HUMAN	wc09c08.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2314670 3'
1383	6380	11430	8.53	5.0E-93	AB74184.1	EST_HUMAN	wc09c08.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2314670 3'
3162	8178	13200	4.58	5.0E-93	X04201.1	NT	Human skeletal muscle 1.3 kb mRNA for tropomyosin
86	5163		5.69	4.0E-93	AA459933.1	EST_HUMAN	z60e09.s1 Soares testis NIH_MGC_44 Homo sapiens cDNA clone IMAGE:785688 3' similar to SW:CLPA_RAT
442	5479	10496	1.62	4.0E-93	4557879	NT	P37397 CALPONIN, ACIDIC ISOFORM 1
442	5479	10497	1.62	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
763	5784	10812	4.03	4.0E-93	7657454	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
763	5784	10813	4.03	4.0E-93	7657454	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
1164	6167	11201	1.25	4.0E-93	8923658	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
1932	6818	12017	3.59	4.0E-93	AF047677.1	NT	Homo sapiens hypothetical protein FLJ20731 (FLJ20731), mRNA
2183	7162	12282	0.93	4.0E-93	AF157476.1	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5
2533	7498	12618	1.01	4.0E-93	7656872	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
3487	8495	13512	0.79	4.0E-93	7705396	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
3935	8934	13927	5.14	4.0E-93	4504854	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
4863	8495	13512	0.83	4.0E-93	7705396	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
3567	8574	13579	19.66	3.0E-93	BF690830.1	EST_HUMAN	602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
3567	8574	13580	19.68	3.0E-93	BF690830.1	EST_HUMAN	602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
180	5254	10265	31.68	2.0E-93	AB015610.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds
180	5254	10266	31.68	2.0E-93	AB015610.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds
321	5376	10386	9.39	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
322	6376	10388	6.39	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
2072	7054	12184	1.86	2.0E-93	U40763.1	NT	Human Cdk-associated RS cyclophilin CARS-Cyp mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2416	7387	12507	1.74	2.0E-93	BE252982.1	EST_HUMAN	601117586F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3358220 5'
4986	9943	14920	1.01	2.0E-93	BE253201.1	EST_HUMAN	601116810F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357243 5'
102	5179	10189	2.66	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
102	5179	10190	2.66	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
514	5549	10554	17.48	1.0E-93	7657016	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
595	5626	10625	3.67	1.0E-93	AI146755.1	EST_HUMAN	cy64b08.x1 NCL_CGAP_CL11 Homo sapiens cDNA clone IMAGE:1672503 3' similar to TR:Q62384 Q62384 ZINC FINGER PROTEIN.
881	5880	10921	7.39	1.0E-93	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1217	6216	11258	8.15	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1217	6216	11257	8.15	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1325	6323	11370	1.13	1.0E-93	AB046783.1	NT	Homo sapiens mRNA for KIAA1563 protein, partial cds
1327	6325	11372	3.03	1.0E-93	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2276	7252	12370	5.14	1.0E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2394	7365	12487	12.91	1.0E-93	AF05086.1	NT	Homo sapiens MHC class 1 region
2435	7406		1.31	1.0E-93	AL137200.1	NT	Novel human gene mapping to chromosome 1
2749	6275	11316	1.39	1.0E-93	BE297369.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
2749	6275	11316	1.39	1.0E-93	BE297369.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
2863	7883	12803	3.34	1.0E-93	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
3144	8160		1.76	1.0E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
4305	9297	14283	2.36	1.0E-93	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3856	8858	13864	3.44	6.0E-94	AF142482.1	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
1806	6797	12664	38.53	4.0E-94	LO5094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
2596	7549	12664	1.13	4.0E-94	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3587	8594	13598	1.02	4.0E-94	AW197851.1	EST_HUMAN	xn89f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
3587	8594	13599	1.02	4.0E-94	AW197851.1	EST_HUMAN	xn89f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
4579	9587	14556	3.55	4.0E-94	AI591312.1	EST_HUMAN	tw11f10.x1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2259403 3' similar to TR:Q15285 Q15285 PROTEIN TYROSINE PHOSPHATASE
607	5634	10635	3.13	3.0E-94	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
711	5735	10751	1.52	3.0E-94	4502508	NT	Homo sapiens complement component 5 (C5) mRNA
1701	6636	11772	3.56	3.0E-94	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1701	6636	11773	3.56	3.0E-94	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1735	6730	11807	6.42	3.0E-94	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA

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4065	9059	14046	0.67	3.0E-94	AA464805.1	EST_HUMAN	zw63g08.r1 Soares_tetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:774782 5'
5051	10022	14991	0.7	3.0E-94	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
146	5214	10228	2.88	1.0E-94	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3015	8032	13042	2.59	1.0E-94	BE293433.1	EST_HUMAN	60111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
3015	8032	13043	2.59	1.0E-94	BE253433.1	EST_HUMAN	60111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
4233	9227	14211	1.7	1.0E-94	9506692	NT	Homo sapiens hypothetical protein (FLJ20746), mRNA
1447	6444	11503	5.95	9.0E-95	AF027302.1	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3082	8098	13112	1.09	9.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3082	8098	13113	1.09	9.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
4406	9397	14380	3.37	8.0E-95	AI700998.1	EST_HUMAN	w609e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
4406	9397	14381	3.37	8.0E-95	AI700998.1	EST_HUMAN	w609e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
273	5332	10344	10.53	7.0E-95	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
273	5332	10345	10.53	7.0E-95	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4241	9235	14219	5.66	7.0E-95	M95708.1	NT	Homo sapiens Ly-6-like protein (CD59) mRNA, complete cds
4289	9281	11662	1.4	7.0E-95	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1605	6601	11662	3.13	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1605	6601	11663	3.13	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1901	8886	11982	3.11	2.0E-95	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
1804	8891	11986	1.74	2.0E-95	BE393873.1	EST_HUMAN	60131216F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658862 5'
2359	7333	12449	1.55	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2359	7333	12450	1.55	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2396	7367	12488	2.79	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2442	7412	12528	1.84	2.0E-95	4758423	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
3084	8100	13115	1.95	2.0E-95	AF015452.1	NT	Homo sapiens Ubrin-gamma mRNA, complete cds
3484	8492	13508	2.78	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3484	8492	13509	2.78	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3537	8543	13549	1.17	2.0E-95	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
3684	8669	13674	1	2.0E-95	AI280264.1	EST_HUMAN	qm01c02.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1880546 3' similar to WP:T23G7.4 CE03705;
4238	9230	14213	1.61	2.0E-95	7657185	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA

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4873	9852	14827	2.85	2.0E-95	7661978	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4917	9895	14869	0.92	2.0E-95	AA447831.1	EST_HUMAN	z11407.1 Soares fetal Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 5'
4917	9895	14870	0.92	2.0E-95	AA447831.1	EST_HUMAN	z11407.1 Soares fetal Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 5'
439	7720	10483	3.42	8.0E-98	BE907607.1	EST_HUMAN	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899761 5'
439	7720	10484	3.42	8.0E-98	BE907607.1	EST_HUMAN	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899761 5'
3813	8816	13822	1.16	7.0E-98	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
2198	7176	12299	2.4	6.0E-96	BE171984.1	EST_HUMAN	MRO-HT0559-260200-002-d07 HT0559 Homo sapiens cDNA
3244	8257	13278	0.86	6.0E-96	BE171984.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
3402	8411	13437	37.31	6.0E-98	M28873.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase pseudogene 3'end
318	5373	10382	3.23	5.0E-98	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
832	5851	10889	3.33	5.0E-96	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
832	5851	10890	3.33	5.0E-98	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
2845	7510		2.15	5.0E-96	11418767	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
4748	9733		1.28	5.0E-96	X60812.1	NT	H sapiens DNA for monamine oxidase type A (7) (partial)
4067	9061		10.55	3.0E-96	H68656.1	EST_HUMAN	yr87h12.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:212327 5'
412	5449		4.94	2.0E-96	4503098	NT	Homo sapiens chondroclon sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
738	5761	10784	1.2	2.0E-96	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1756	6749	11832	1.81	2.0E-96	7708205	NT	Homo sapiens CGI-201 protein (LOC51340), mRNA
4613	9599	14585	2.68	2.0E-96	BE148074.1	EST_HUMAN	RC3-HT0230-040500-110-g02 HT0230 Homo sapiens cDNA
663	5689	10698	2.97	1.0E-96	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1743	6738	11814	4.56	1.0E-96	AW955054.1	EST_HUMAN	EST367124 MAGC resequences, MAGC Homo sapiens cDNA
1743	6738	11815	4.56	1.0E-96	AW955054.1	EST_HUMAN	EST367124 MAGC resequences, MAGC Homo sapiens cDNA
2204	7705	12305	1.95	1.0E-96	U51472.2	NT	Felis catus superfast myosin heavy chain (amyHC) mRNA, complete cds
925	6942	10976	3.84	4.0E-97	BE004436.1	EST_HUMAN	CMO-BN0106-170300-293-e06 BN0106 Homo sapiens cDNA
1867	6856	11944	1.34	4.0E-97	5453572	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
241	5302	10312	2.28	3.0E-97	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
863	5882	10923	9.5	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
863	5882	10924	9.5	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1415	7747	11473	1.64	3.0E-97	4758813	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
2371	7706	12462	2.66	3.0E-97	U36255.1	NT	Human beta-prime-adaplin (BAM22) gene, exon 7
3188	8202	13224	1.14	3.0E-97	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
4635	9820	14612	35.24	1.0E-97	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA

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890	5908	10948	6.71	9.0E-98	BE090973.1	EST_HUMAN	PM4-BT0724-010400-008-e12 BT0724 Homo sapiens cDNA
1257	6255	11297	1.1	9.0E-98	8393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
5021	6992	14866	1.03	9.0E-98	11418594	NT	Homo sapiens FSH primary response (LRPR1, rat) homolog 1 (FSHPRH1), mRNA
24	5104		4.32	8.0E-98	AJ251158.1	NT	Homo sapiens partial MICB gene for MHC class I chain-related protein B, exons 2-3 and joined CDS
1529	6526	11584	1.06	8.0E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1529	6526	11585	1.06	8.0E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1688	6684	11759	3.31	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1688	6684	11760	3.31	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3706	8710	13713	6.04	8.0E-98	JO4469.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2113	7093	12207	1.06	3.0E-98	AJ403124.1	EST_HUMAN	Human mitochondrial creatine kinase (CKMT) gene, complete cds
2534	7499	12619	1.4	3.0E-98	AB014607.1	NT	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone IB
2676	7634		2.13	3.0E-98	AA077498.1	EST_HUMAN	Homo sapiens mRNA for KIAA0707 protein, partial cds
726	5749	10770	2.43	2.0E-98	BE261694.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
2028	7009	12115	2.25	2.0E-98	BE294281.1	EST_HUMAN	601149486F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3602245 5'
2176	7155	12275	2.4	2.0E-98	AL163202.2	NT	601172658F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528134 5'
3989	8987	13973	0.94	2.0E-98	8923308	NT	Homo sapiens chromosome 21 segment HS21C002
4172	9167	14164	0.88	2.0E-98	AF032897.1	NT	Homo sapiens hypothetical protein FLJ20333 (FLJ20333), mRNA
4214	9207	14186	3.27	2.0E-98	4758331	NT	Homo sapiens poliovirus channel subunit (HERG-3) mRNA, complete cds
4680	9665	14646	1.61	2.0E-98	AF218902.1	NT	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA
4680	9665	14647	1.61	2.0E-98	AF218902.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
403	5439	10459	91.85	1.0E-98	AJ862007.1	EST_HUMAN	Homo sapiens attractin precursor (ATRIN) gene, exon 16
452	5489	10504	2.47	1.0E-98	AW898611.1	EST_HUMAN	tw36b04.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2261743 3' similar to SW:RL2B_HUMAN
1761	6753	11838	68.95	1.0E-98	N49818.1	EST_HUMAN	PM0-BN0065-100300-001-c06 BN0065 Homo sapiens cDNA
2089	7051	12159	1.5	6.0E-98	11430555	NT	P29316 60S RIBOSOMAL PROTEIN L23A
2089	7051	12160	1.5	6.0E-98	11430555	NT	PM0-BN0065-100300-001-c06 BN0065 Homo sapiens cDNA
4605	9593	14578	1.1	6.0E-98	4502860	NT	y23105.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243585 5' similar to
1924	6910	12005	0.92	5.0E-98	Y11365.1	NT	PIR:S54204 S54204 ribosomal protein L29 - human
4432	9422	14408	1.25	5.0E-98	AF008660.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA
4586	9574	14564	1.82	5.0E-98	AF265555.1	NT	Homo sapiens cyclin-rich repeat-containing protein S52 precursor, (LOC51232), mRNA
4586	9574	14565	1.82	5.0E-98	AF265555.1	NT	Homo sapiens CD34 antigen (CD34) mRNA
							H. sapiens IMPA gene, exon 8
							Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
							Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
							Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1220	8220		21.29	2.0E-99	AW274792.1	EST_HUMAN	xp09906.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739874 3' similar to gb:M31212 MYOSIN
3184	8200	13223	2.08	2.0E-99	M30838.1	NT	LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM (HUMAN); Human Ku (p70/p80) subunit mRNA, complete cds
4412	9402	14387	2.65	2.0E-99	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
313	5368	10378	1.21	1.0E-99	AF114487.1	NT	Homo sapiens Intersectin long isoform (ITSN) mRNA, complete cds
378	5425	10440	1.23	1.0E-99	11526150	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
1366	6383	11447	8.91	1.0E-99	M30838.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1525	6522	11578	3.27	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1525	6522	11578	3.27	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1886	6875	11964	1.12	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
1886	6875	11965	1.12	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
3011	8028	13039	1.27	1.0E-99	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
4255	9249	14233	2.45	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4255	9249	14234	2.45	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
1	5083	10067	1.68	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2	5083	10067	1.64	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
67	5146	10151	1.24	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
67	5146	10152	1.24	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
85	5162	10174	2.54	1.0E-100	AW275237.1	EST_HUMAN	xv78b11.x1 NCI_CGAP_Brn53 Homo sapiens cDNA clone IMAGE:2824605 3'
168	5233	10243	0.69	1.0E-100	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
315	5370	10381	1.05	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
341	5393	10400	1.8	1.0E-100	T05087.1	EST_HUMAN	EST02975 Fetal brain, Striatum (cat#939206) Homo sapiens cDNA clone HFBOR32
434	5472		1.98	1.0E-100	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
486	5523		19.01	1.0E-100	X89831.1	NT	G.gorilla DNA for ZNF80 gene homolog
508	5541	10547	1.36	1.0E-100	BE180609.1	EST_HUMAN	RC3-HT0825-040500-022-b09 HT0825 Homo sapiens cDNA
1003	6013	11042	2.46	1.0E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1003	6013	11043	2.46	1.0E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1514	6512		1.64	1.0E-100	AW207555.1	EST_HUMAN	UI-H-B11-afk-c-07-0-J1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3'
1519	6516	11573	1.15	1.0E-100	AI200857.1	EST_HUMAN	qf62T09.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1784633 3' similar to SW:CYT_COTJA
1827	6817	11911	1.44	1.0E-100	AB032894.1	NT	P81061 CYSTATIN ; Homo sapiens mRNA for KIAA1168 protein, partial cds
2634	7594	12707	1.52	1.0E-100	11418976	NT	Homo sapiens KIAA0857 protein (KIAA0857), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2652	7871		4.15	1.0E-100	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
4089	8083	14074	1.57	1.0E-100	AF057354.1	NT	Homo sapiens myotubularin-related protein 1a mRNA, partial cds
4114	9108	14093	2.28	1.0E-100	4503792	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
4920	8898	14872	3.82	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
4920	8898	14873	3.82	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
76	5154	10164	1.88	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
76	5154	10165	1.88	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
677	5702	10710	2.59	1.0E-101	AB007915.2	NT	Homo sapiens mRNA for KIAA0446 protein, partial cds
684	5718	10735	6.32	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
694	5718	10736	6.32	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
762	5783	10811	4.64	1.0E-101	7657454	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
843	5862	10902	3.85	1.0E-101	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylaminimidazole synthetase (GART) mRNA
970	5985	11020	34.38	1.0E-101	BF681218.1	EST_HUMAN	602156474F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297291 5'
1035	6045	11074	1.9	1.0E-101	A1221878.1	EST_HUMAN	gg99a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
1548	6546	11606	2.07	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1548	6546	11607	2.07	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1707	6702	11779	1	1.0E-101	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1707	6702	11780	1	1.0E-101	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1905	6882	11987	1.32	1.0E-101	4502996	NT	Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1) mRNA
2003	6986	12090	2.61	1.0E-101	BE843070.1	EST_HUMAN	RC3-ST0281-160600-018-h09 ST0281 Homo sapiens cDNA
2288	7767	12381	0.97	1.0E-101	5728962	NT	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA
2541	7506	12625	6.73	1.0E-101	X72893.1	NT	H. sapiens EWS gene, exon 5
2670	7628	12741	5.15	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
2670	7628	12742	5.15	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
2884	7803		12.51	1.0E-101	AJ252312.1	NT	Homo sapiens genomic downstream Rhesus box
3130	8146	13167	2.4	1.0E-101	4885270	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA
3167	8183		2.78	1.0E-101	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
3296	8307	13332	2.01	1.0E-101	AW963556.1	EST_HUMAN	EST377628 IMAGE resequences, MAGI Homo sapiens cDNA
3316	7628	12741	3.42	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
3316	7628	12742	3.42	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
3785	8798	13792	5.05	1.0E-101	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
4888	9847	14823	1.61	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
4888	9847	14824	1.61	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
40	5120	10108	0.96	1.0E-102	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
339	5391	10397	4.55	1.0E-102	AL183303.2	NT	Homo sapiens chromosome 21 segment HS21C103
615	5642	10845	0.83	1.0E-102	BE262470.1	EST_HUMAN	601108292F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344326 5'
766	5787	10816	0.81	1.0E-102	4557534	NT	Homo sapiens down-regulated in adenoma (DRA) mRNA
1100	6107	11137	3.79	1.0E-102	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1249	6247	11287	1.82	1.0E-102	11437148	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1249	6247	11288	1.82	1.0E-102	11437148	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1394	6391	11444	373.13	1.0E-102	BE408447.1	EST_HUMAN	601298992F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629901 5'
2246	7223	12342	3.39	1.0E-102	AI124669.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95.1
2246	7223	12343	3.39	1.0E-102	AI124669.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95.1
2786	7607	12824	0.69	1.0E-102	11419442	NT	Homo sapiens peroxisome biogenesis factor 1 (PEX1), mRNA
2891	8009	13022	1.4	1.0E-102	7661978	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
3060	8077	13069	2.88	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
3060	8077	13090	2.88	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
4111	9105	14091	1.63	1.0E-102	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4287	9278	14267	2.09	1.0E-102	BE251310.1	EST_HUMAN	601107843F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343882 5'
4948	9925	14903	1.17	1.0E-102	R68488.1	EST_HUMAN	y32c04.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140834 5'
68	5147	10153	1.86	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
68	5147	10154	1.86	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
89	5176	10186	7.11	1.0E-103	D87076.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
208	5272	10284	9	1.0E-103	5453793	NT	Homo sapiens nuclear protein (KKE/D repeat) (NOP56) mRNA
966	5981	11013	0.87	1.0E-103	AJ278348.1	NT	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)
1224	6223	11269	8.76	1.0E-103	BE877541.1	EST_HUMAN	601485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887876 5'
1561	6558	11620	3.06	1.0E-103	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
1870	6859	11947	0.99	1.0E-103	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
1930	6916	12013	1.28	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
1930	6916	12014	1.28	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2242	7219	12338	2.16	1.0E-103	AU134991.1	EST_HUMAN	AU134991 PLACE1 Homo sapiens cDNA clone PLACE1000965 5'
2383	7354	12476	1.58	1.0E-103	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
2547	7512	12630	1.26	1.0E-103	N32770.1	EST_HUMAN	yw91408.at Soares placenta_8to9weeks_2NbHP8c9W Homo sapiens cDNA clone IMAGE:259599 3'
2895	8013		2.58	1.0E-103	BE744722.1	EST_HUMAN	601573113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834315 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3295	8306	13331	4.02	1.0E-103	AW288245.1	EST_HUMAN	UI-H-BW0-ajh-h-11-QJL.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:27933165 3'
3355	8363	13379	1.23	1.0E-103	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
3669	8674		9	1.0E-103	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
3704	8708	13711	1.2	1.0E-103	AA485663.1	EST_HUMAN	ab10d12.s1 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element:
3739	8743	13743	1.26	1.0E-103	11430876	NT	Homo sapiens neuropilin 1 (NRP1), mRNA
3897	8897	13895	2.44	1.0E-103	T23683.1	EST_HUMAN	seq340 b4HB3MA-Cot109+10-Bio Homo sapiens cDNA clone b4HB3MA-Cot109+10-Bio-7 3'
4846	8831	14628	3.54	1.0E-103	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
233	5288	10305	4.73	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072_r1 564 (synonym: hibr2) Homo sapiens cDNA clone DKFZp564H1072 5'
233	5296	10306	4.73	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072_r1 564 (synonym: hibr2) Homo sapiens cDNA clone DKFZp564H1072 5'
1849	6838	11927	1.93	1.0E-104	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2131	7111	12224	5.4	1.0E-104	AA132875.1	EST_HUMAN	zo22c08.s1 Strategene colon (#837204) Homo sapiens cDNA clone IMAGE:587626 3' similar to gb:Z14116.maf1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
2141	7120	12236	5.95	1.0E-104	BE744828.1	EST_HUMAN	601577480F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926438 5'
2308	7283	12402	3.55	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-112 CT0249 Homo sapiens cDNA
2308	7283	12403	3.55	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-112 CT0249 Homo sapiens cDNA
2370	7343	12461	6.02	1.0E-104	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2430	7401	12519	1.36	1.0E-104	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2430	7401	12520	1.36	1.0E-104	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), complete cds
2800	7820	12837	6.92	1.0E-104	M34871.1	NT	Human lymphocytic antigen OD59/MEM43 mRNA, complete cds
2846	7866	13227	2.57	1.0E-104	Y11151.1	NT	H. sapiens gene encoding phenylpyruvate tautomerase II
3189	8205	13227	0.95	1.0E-104	AA133928.1	EST_HUMAN	AU133928 OVARC1 Homo sapiens cDNA clone OVARC1000936 5'
3307	8318	13948	1.84	1.0E-104	AA319436.1	EST_HUMAN	EST21658 Adrenal gland tumor Homo sapiens cDNA 5' end
3639	8841	13948	1.14	1.0E-104	AB032985.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
4008	9004	13992	1.24	1.0E-104	F11745.1	EST_HUMAN	HSC3A071 normalized infant brain cDNA Homo sapiens cDNA clone c-31807
4252	9246	14230	4.98	1.0E-104	X02761.1	NT	Human mRNA for fibronectin (FN precursor)
4477	9467	14446	1.5	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
4477	9467	14447	1.5	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
276	7691	10348	3.85	1.0E-105	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
422	5080	10064	18.42	1.0E-105	4505160	NT	Homo sapiens Meis1 (mouse) homolog (MEIS1) mRNA
589	5820	10618	6.63	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
589	5820	10619	6.63	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1640	8637		5.48	1.0E-105	AB020981.1	NT	Homo sapiens mRNA for cyclin B2, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1667	6663	11738	1.04	1.0E-105	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1765	6777	11869	1.78	1.0E-105	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1885	6874	11863	1.62	1.0E-105	D50918.1	NT	Human mRNA for KIAA0128 gene, partial cds
2126	7106	12220	5.92	1.0E-105	AA318369.1	EST_HUMAN	EST20609 Spleen 1 Homo sapiens cDNA 5' end similar to autoimmune antigen Ku, p70/p80 subunit
2260	7237		1.56	1.0E-105	BE8891768.1	EST_HUMAN	601434491F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919511 5'
2849	7609		0.96	1.0E-105	AA584808.1	EST_HUMAN	no10d05.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100265 3'
2937	7956		3.39	1.0E-105	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
3252	8265	13286	1.32	1.0E-105	BF347753.1	EST_HUMAN	602022595F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158143 5'
3252	8265	13287	1.32	1.0E-105	BF347753.1	EST_HUMAN	602022595F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158143 5'
3981	8979	13984	6.06	1.0E-105	AW981688.1	EST_HUMAN	EST373761 MAGI Mage resequences, MAGI Homo sapiens cDNA
4781	9765		4.42	1.0E-105	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
4934	9911	14889	0.92	1.0E-105	AB018339.1	NT	Homo sapiens mRNA for KIAA0786 protein, partial cds
4974	9950	14928	1.08	1.0E-105	AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
4987	9961	14938	0.67	1.0E-105	AW966015.1	EST_HUMAN	EST378088 MAGI Mage resequences, MAGI Homo sapiens cDNA
150	5216		1.69	1.0E-106	AW503208.1	EST_HUMAN	UI-HF-BN0-akt-g-07-q-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
205	5269	10282	2.72	1.0E-106	AI565065.1	EST_HUMAN	iq79c01.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2215008 3'
537	5572	10578	1.61	1.0E-106	AW965556.1	EST_HUMAN	EST377629 MAGI Mage resequences, MAGI Homo sapiens cDNA
602	5631	10631	8.07	1.0E-106	J00148.1	NT	Human dihydrofolate reductase pseudogene (psi-hd1)
603	5631	10631	6.16	1.0E-106	J00146.1	NT	Human dihydrofolate reductase pseudogene (psi-hd1)
1492	6490	11545	1.78	1.0E-106	AF145712.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
1662	6658	11732	3.2	1.0E-106	U48724.1	NT	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
1681	6677	11751	2.79	1.0E-106	U04510.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 41
1767	6769	11845	3.22	1.0E-106	AA627446.1	EST_HUMAN	ng41c05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:837352 3' similar to contains element
1767	6759	11846					LTR3 repetitive element
2063	7045	12153	1.25	1.0E-106	BE144286.1	EST_HUMAN	ng41c05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:837352 3' similar to contains element
2253	7230	12349	10.26	1.0E-106	4504184	NT	LTR3 repetitive element
2432	7403	12522	1.47	1.0E-106	AF003528.1	NT	MRO-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
2525	7491	12611	1	1.0E-106	U64875.2	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2527	7493	12613	1.49	1.0E-106	BE260201.1	EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2683	7641	12757	10	1.0E-106	AI276526.1	EST_HUMAN	Homo sapiens sperm membrane protein BS-63 mRNA, complete cds
2752	8404	11462	7.19	1.0E-106	4504184	NT	601149783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502481 5'
							q17b10.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878307 3'
							Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2752	6404	11463	7.19	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2805	7825	12840	1.79	1.0E-108	BE384286.1	EST_HUMAN	601272675F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3613818 5'
2870	7889	12910	4.45	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1328 protein, partial cds
2870	7889	12911	4.45	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1328 protein, partial cds
3107	8123	13141	2.41	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3107	8123	13142	2.41	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3356	8364	13380	0.99	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3356	8364	13381	0.99	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3714	8718	13719	0.92	1.0E-106	AF001445.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 2
3926	8926	13916	10.11	1.0E-108	AW974650.1	EST_HUMAN	EST388875 IMAGE resequences; MAGN Homo sapiens cDNA
3926	8926	13917	10.11	1.0E-108	AW974650.1	EST_HUMAN	EST388875 IMAGE resequences; MAGN Homo sapiens cDNA
3944	8942	13932	1.74	1.0E-106	5729729	NT	Homo sapiens AP15-like 1 (AP15L1), mRNA
4470	9460	14439	0.67	1.0E-106	BE144286.1	EST_HUMAN	MRO-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
4741	9726	14711	1.39	1.0E-106	U31520.1	NT	Human alpha mannosidase II mRNA, complete cds
234	5297		3.3	1.0E-107	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
262	5321		1.47	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
624	5651	10655	2.22	1.0E-107	AF155103.1	NT	Homo sapiens NY-REN-25 antigen mRNA, partial cds
803	5824	10854	1.94	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
875	5893	10834	1.25	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
954	5970	11003	8.1	1.0E-107	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1259	6257	11300	2.22	1.0E-107	AB032283.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1536	6534	11593	8.86	1.0E-107	BF087405.1	EST_HUMAN	QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA
1713	6708	11784	4.61	1.0E-107	AF136275.1	NT	Homo sapiens cathepsin Z precursor (CTSZ) gene, exon 3
1804	6795	11885	2.87	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1804	6795	11886	2.87	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2146	7125	12242	1.06	1.0E-107	U13729.1	NT	Human dipeptidyl peptidase IV (CD26) gene, exon 20
2301	7276	12395	4.22	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2301	7276	12396	4.22	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2463	7432	12550	1.65	1.0E-107	BE732480.1	EST_HUMAN	601567619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2463	7432	12551	1.65	1.0E-107	BE732480.1	EST_HUMAN	601567619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2938	7957	12974	3.71	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2938	7957	12975	3.71	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3026	8043	13052	7.53	1.0E-107	5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3736	8740	13738	5.33	1.0E-107	AF020871.1	NT	Homo sapiens myotubularin (MTM1) gene, exon 9
840	5957	10980	2.88	1.0E-108	BE286042.1	EST_HUMAN	601177018F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532348 5'
1246	6244	11284	5.83	1.0E-108	Y18000.1	NT	Homo sapiens NF2 gene
2025	7008	12114	1.65	1.0E-108	BF028728.1	EST_HUMAN	601871914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'
2360	7334	12451	12.25	1.0E-108	BE206694.1	EST_HUMAN	bb25b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963899 3' similar to gb:X53777 60S RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexokinase mRNA, complete cds (MOUSE);
4033	8029	14017	1.15	1.0E-108	AW664438.1	EST_HUMAN	hi12a11.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972060 3' similar to SW:3BP1_MOUSE P85194 SH3-BINDING PROTEIN 3BP-1;
4394	9385	14367	3.04	1.0E-108	U72981.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4394	8385	14368	3.04	1.0E-108	U72981.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4659	9844	14632	3.68	1.0E-108	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4765	9749	14737	0.88	1.0E-108	AW504789.1	EST_HUMAN	U1-HF-BN0-ahr-04-Q-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080168 5'
4791	9776	14759	2.91	1.0E-108	AJ008005.1	NT	Homo sapiens PSN1 gene, alternative transcript
4962	8939	14918	0.95	1.0E-108	5031824	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
4988	8962	14939	0.72	1.0E-108	Y12490.1	NT	Homo sapiens mRNA for Golgi-associated microtubule-binding protein (GMAP-210)
43	5123	10111	2.46	1.0E-109	AW803116.1	EST_HUMAN	IL2-UM0077-260400-078-D08 UM0077 Homo sapiens cDNA
66	5145	10150	3.94	1.0E-109	D86974.1	NT	Human mRNA for KIAA0220 gene, partial cds
218	5281	10282	0.76	1.0E-109	11422486	NT	Homo sapiens hypothetical protein FLJ11318 (FLJ11318), mRNA
228	5288	10296	7.69	1.0E-109	11438391	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
484	5501	10511	9.2	1.0E-109	4507712	NT	Homo sapiens tetraicosapeptide repeat domain 2 (TTC2) mRNA
593	5624	10623	15.28	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0899 protein, partial cds
593	5624	10624	16.28	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0899 protein, partial cds
1183	6185	11222	83.77	1.0E-109	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1184	6185	11222	72.21	1.0E-109	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1510	6508	11584	1.52	1.0E-109	BE283673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959836 5'
1510	6508	11565	1.52	1.0E-109	BE283673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959836 5'
1836	6826	11914	5.54	1.0E-109	D13643.2	NT	Homo sapiens mRNA for KIAA0018 protein, partial cds
2181	7160	12280	2.32	1.0E-109	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2189	7168	12288	4.31	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
2549	7514	12632	4.09	1.0E-108	A1023238.1	EST_HUMAN	ow85a01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654538 3' similar to TR:O02197 002197 CIRCULATING CATHODIC ANTIGEN.;
2549	7514	12633	4.09	1.0E-109	A1023238.1	EST_HUMAN	ow85a01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654538 3' similar to TR:O02197 002197 CIRCULATING CATHODIC ANTIGEN.;

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2550	7615	12634	2.41	1.0E-109	4504206	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
2984	8002	13014	1.32	1.0E-109	N85190.1	EST_HUMAN	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC
3304	8315	13341	1.43	1.0E-109	AW893192.1	EST_HUMAN	FINGER PROTEIN ZNF43
3304	8315	13342	1.43	1.0E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150-110 NN0009 Homo sapiens cDNA
3440	8448	13474	1	1.0E-109	AF240698.1	NT	CM3-NN0009-190400-150-110 NN0009 Homo sapiens cDNA
3751	8755		2.78	1.0E-109	BE146144.1	EST_HUMAN	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
							MRO-HT0209-110400-108-a04 HT0209 Homo sapiens cDNA
4023	9019	14006	4.42	1.0E-109	AI655417.1	EST_HUMAN	ts98e06.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:239330 3' similar to WP:F53A2.8
4038	9034	14022	0.94	1.0E-109	AA682274.1	EST_HUMAN	CE16100 ;
4038	9034	14022	0.94	1.0E-109	AA682274.1	EST_HUMAN	nu93c12.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1218282 3' similar to SW:GTT2_HUMAN
4038	9034	14022	0.94	1.0E-109	AA682274.1	EST_HUMAN	P30712 GLUTATHIONE S-TRANSFERASE THETA 2 ;
4280	9273	14262	2.85	1.0E-109	4504206	NT	nu93c12.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1218282 3' similar to SW:GTT2_HUMAN
4489	9459	14438	1.07	1.0E-109	7662083	NT	P30712 GLUTATHIONE S-TRANSFERASE THETA 2 ;
3	5084	10068	0.8	1.0E-110	7549804	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
38	5118	10105	3.85	1.0E-110	5803073	NT	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
38	5118	10106	3.85	1.0E-110	5803073	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
109	5084	10068	0.78	1.0E-110	7549804	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
292	5349	10362	0.83	1.0E-110	D87291.1	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
523	5558	10581	0.78	1.0E-110	U84550.1	NT	Human mRNA for inward rectifier potassium channel, complete cds
1161	6165	11189	0.8	1.0E-110	5031620	NT	Human dystrobrevin (DTN) gene, exon 20
1260	6258	11301	1.42	1.0E-110	AB032253.1	NT	Homo sapiens calcitonin receptor-like (CALCRL) mRNA
1879	6888	11957	0.92	1.0E-110	BE378477.1	EST_HUMAN	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
2005	6988		1.45	1.0E-110	BF508896.1	EST_HUMAN	601237645F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609883 5'
2787	7788		2	1.0E-110	4503068	NT	UI-H-B14-acs-b-05-Q-UJ.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
2861	8258	11301	1.29	1.0E-110	AB032253.1	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
3013	8030		1.07	1.0E-110	U78027.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
4080	8074	14062	2.55	1.0E-110	M15918.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
4500	9490	14466	2.09	1.0E-110	AJ017213.1	EST_HUMAN	Human autolysate antigen small nuclear ribonucleoprotein E pseudogene
4520	9510	14494	3.28	1.0E-110	AU117812.1	EST_HUMAN	alpha32B10.x1 Sceres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627863 3' similar to
4814	9798		2.3	1.0E-110	7662441	NT	SW:N121_RAT_P52591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ;
							AUT117812 HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5'
							Homo sapiens KIAA1002 protein (KIAA1002), mRNA

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
174	5238		43.9	1.0E-111	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
196	5260	10273	1.07	1.0E-111	4758807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
725	5748		2.71	1.0E-111	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
734	5757	10779	3.66	1.0E-111	8393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
914	5930	10965	2.28	1.0E-111	M25142.1	NT	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34
1589	6586	11848	1.57	1.0E-111	7662177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
4047	9043	14032	1.17	1.0E-111	7661569	NT	Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA
4203	9186	14178	4.64	1.0E-111	K02268.1	NT	Human enkephalin B (enkeB) gene, exon 4 and 3' flank and complete cds
605	5632	10632	0.87	1.0E-112	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
606	5633	10633	4.82	1.0E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
609	5633	10634	4.82	1.0E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
626	5653	10657	1.33	1.0E-112	BF509039.1	EST_HUMAN	UI-H-B14-aot-g-04-Q-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
626	5653	10658	1.33	1.0E-112	BF509039.1	EST_HUMAN	UI-H-B14-aot-g-04-Q-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
986	6001	11032	1.84	1.0E-112	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1045	6055	11083	2.53	1.0E-112	P62742	SWISSPROT	ZINC FINGER PROTEIN 135
1645	6641	11711	3.11	1.0E-112	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1645	6641	11712	3.11	1.0E-112	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2436	7407	12524	1.26	1.0E-112	BE86859.1	EST_HUMAN	601442674F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846858 5'
3004	8022		0.72	1.0E-112	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3171	8187	13208	1.07	1.0E-112	BE083092.1	EST_HUMAN	RC2-BT0642-030400-021-d09 BT0642 Homo sapiens cDNA
3171	8187	13208	1.07	1.0E-112	BE083092.1	EST_HUMAN	RC2-BT0642-030400-021-d09 BT0642 Homo sapiens cDNA
3760	8793	13798	0.71	1.0E-112	AB037832.1	EST_HUMAN	MR2-BT0590-080300-113-f09 BT0590 Homo sapiens cDNA
4608	8995	14580	5.12	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
4608	8995	14581	5.12	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
733	5756	10777	7.13	1.0E-113	AJ365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
733	5756	10778	7.13	1.0E-113	AJ365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
828	5945	10979	7.7	1.0E-113	M11865.1	NT	Human X-linked phosphoglycerate kinase gene, exon 8
1509	6507	11663	3.94	1.0E-113	AJ365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
1899	7702	11980	1.45	1.0E-113	AF240776.1	NT	Homo sapiens eIF4E transporter mRNA, complete cds
3057	8074	13087	2.18	1.0E-113	AJ223948.1	NT	Homo sapiens mRNA for putative RNA helicase, 3' and
59	5139	10138	0.76	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
59	5139	10139	0.76	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
59	5139	10140	0.76	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
637	5665	10669	5.07	1.0E-114	T70551.1	EST_HUMAN	yt15c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109288 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN); contains Alu repetitive element;
1054	6063	11093	3.1	1.0E-114	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1294	6292	11338	3.85	1.0E-114	7657628	NT	Homo sapiens thadoid tumor deletion region protein 1 (RTDR1), mRNA
1602	6598	11659	5.21	1.0E-114	6831094	NT	Homo sapiens mitochromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
1633	6630	11699	11.15	1.0E-114	6679073	NT	Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA
2194	7173	12284	1.31	1.0E-114	AB002374.1	NT	Human mRNA for KIAA0376 gene, partial cds
2732	5125	10114	1.1	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
2732	5125	10115	1.1	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3058	8075	13088	2.52	1.0E-114	X04086.1	NT	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3098	8114	13132	1.9	1.0E-114	BE206374.1	EST_HUMAN	601869932F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5'
3809	8909	13905	1.56	1.0E-114	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4266	9259	14249	1.12	1.0E-114	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
4984	9941	14918	1.86	1.0E-114	BE275324.1	EST_HUMAN	601122173F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:33346098 5'
22	5102	10087	11.8	1.0E-115	4758111	NT	Homo sapiens HLA-B associated transcript-1 (D6S61E) mRNA
130	5186	10211	2.72	1.0E-115	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
134	5200		21.78	1.0E-115	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
280	5347	10359	4.49	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA
778	5799	10828	1.42	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
778	5799	10829	1.42	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
780	5801	10831	83.62	1.0E-115	4503794	NT	Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA
1528	6525	11582	1.41	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1528	6525	11583	1.41	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
							Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
1805	6786	11887	0.93	1.0E-115	U78027.1	NT	
2027	7010	12116	1.38	1.0E-115	BE745489.1	EST_HUMAN	601578838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2027	7010	12117	1.38	1.0E-115	BE745489.1	EST_HUMAN	601578838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2236	7213	12330	3.07	1.0E-115	AF231124.1	NT	Homo sapiens testican-1 mRNA, complete cds
2778	7799		2.22	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA
3041	8058	13067	7.57	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3041	8058	13068	7.57	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3392	8400	13426	2.06	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
3929	8929	13920	5.04	1.0E-115	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4144	9139	14123	0.86	1.0E-115	AL137163.1	NT	Novel human gene mapping to chromosome X
4278	9271	14260	1.49	1.0E-115	6912659	NT	Homo sapiens sir2-like 3 (SIRT3), mRNA
4313	9305	14289	3.78	1.0E-115	4758279	NT	Homo sapiens EphA4 (EPHA4), mRNA
4459	9449	14429	0.81	1.0E-115	8922435	NT	Homo sapiens hypothetical protein FLJ10466 (FLJ10466), mRNA
4459	9449	14430	0.91	1.0E-115	8922435	NT	Homo sapiens hypothetical protein FLJ10466 (FLJ10466), mRNA
4539	9529	14515	2.4	1.0E-115	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4539	9529	14516	2.4	1.0E-115	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4750	9735	14721	2.89	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4750	9735	14722	2.89	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
567	5600	10599	1.39	1.0E-116	BE275502.1	EST_HUMAN	601121347F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2988875 5'
792	5813	10843	1.45	1.0E-116	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
1951	6937	12038	2.12	1.0E-116	5174478	NT	Homo sapiens pericentrin (PCNT), mRNA
1951	6937	12039	2.12	1.0E-116	5174478	NT	Homo sapiens pericentrin (PCNT), mRNA
1975	6960	12066	1.37	1.0E-116	AU133080.1	EST_HUMAN	AU133080 NT2RP4 Homo sapiens cDNA clone NT2RP4001228 5'
2040	7761	12131	1	1.0E-116	M19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2040	7761	12132	1	1.0E-116	M19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2244	7221	12340	1.16	1.0E-116	5453941	NT	Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1), mRNA
2279	7255		1.38	1.0E-116	U78308.1	NT	Human olfactory receptor pseudo_olfr17-01 (OR17-01) pseudogene, complete cds
2387	7358	12480	1.98	1.0E-116	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
2660	7710	12731	6	1.0E-116	BE889256.1	EST_HUMAN	601613337F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914600 5'
3101	8117	13134	5.82	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
3101	8117	13135	5.82	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
4253	9247	14231	2.06	1.0E-116	5031954	NT	Homo sapiens sodium phosphate transporter 3 (NPT3), mRNA
4707	8692	14675	1.27	1.0E-116	AI907098.1	EST_HUMAN	PM-BT135-070499-016 BT135 Homo sapiens cDNA
4895	8967	14845	0.95	1.0E-116	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
554	5568	10589	1.21	1.0E-117	4826636	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
1081	7738	11101	2.4	1.0E-117	AF124393.1	NT	Mus musculus fragile-X-related protein 1 (Fxr1h) gene, exons 13a through 15
1714	6708	11785	3.05	1.0E-117	AF123320.1	NT	Homo sapiens lymphocyte activation-associated protein mRNA, complete cds
1795	6788	11876	1.83	1.0E-117	M19818.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10
2149	7128	12245	1.3	1.0E-117	AW957699.1	EST_HUMAN	EST369769 MAGE resequences, MAGE Homo sapiens cDNA
2537	7502	12821	1.04	1.0E-117	M63468.1	NT	Human alpha-5 collagen type IV gene, exon 5
3194	8210	13232	1.93	1.0E-117	AA978114.1	EST_HUMAN	qp32c11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1578548 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3884	8885	13885	14.06	1.0E-117	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) (Homo sapiens cDNA 5' end similar to ribosomal protein L29)
4218	9211	14180	2.65	1.0E-117	8659564	NT	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
4444	9434	14417	2.36	1.0E-117	AL042120.1	EST_HUMAN	DKFZp434C1120_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1120 5'
4584	9572	14561	1.11	1.0E-117	X89670.1	NT	H. sapiens mRNA for TPCP16 protein
4584	9572	14562	1.11	1.0E-117	X89670.1	NT	H. sapiens mRNA for TPCP16 protein
4665	9650	14638	11.6	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4665	9650	14639	11.6	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4782	9766	14750	3.85	1.0E-117	AB020673.1	NT	Homo sapiens mRNA for KIAA0868 protein, complete cds
69	5148	10155	11.76	1.0E-118	AF161500.1	NT	Homo sapiens HSPC151 mRNA, complete cds
94	5171	10181	1.94	1.0E-118	AL045854.1	EST_HUMAN	DKFZp434I056_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434I056 5'
513	5548	10553	7.24	1.0E-118	7657016	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
903	7734	10957	6.59	1.0E-118	5174680	NT	Homo sapiens sine oculis homeobox (Drosophila) homolog 1 (SIX1) mRNA
2171	7150	12267	7.75	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2171	7150	12268	7.75	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2171	7150	12269	7.75	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2288	7245	12738	1.9	1.0E-118	AW951728.1	EST_HUMAN	EST363789 MAGC resequences, MAGB Homo sapiens cDNA
2667	7626	12738	3.94	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
2687	7626	12739	3.94	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
3031	8048		4.44	1.0E-118	Y13932.1	NT	Homo sapiens PRKY exon 7
3122	8136	13159	4.93	1.0E-118	A1347694.1	EST_HUMAN	qp01105.x1 NCI CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769 3'
3122	8136	13160	4.93	1.0E-118	A1347694.1	EST_HUMAN	qp01105.x1 NCI CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769 3'
3872	8970	13958	17.63	1.0E-118	D23660.1	NT	Human mRNA for ribosomal protein, complete cds
4569	9557	14545	1.42	1.0E-118	11425793	NT	Homo sapiens KIAA0478 gene product (KIAA0478), mRNA
748	5770	10797	0.93	1.0E-119	AF170492.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
1020	7737	11059	4.3	1.0E-119	7705607	NT	Homo sapiens CGI-105 protein (LOC51011), mRNA
1893	6881	11972	3.42	1.0E-119	AB023147.1	NT	Homo sapiens mRNA for KIAA0930 protein, partial cds
3029	8046	13056	0.92	1.0E-119	8922205	NT	Homo sapiens hypothetical protein FLJ10052 (FLJ10052), mRNA
3847	8849	13857	0.86	1.0E-119	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
299	5356	10368	1.07	1.0E-120	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
1024	6034	11065	2.23	1.0E-120	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1024	6034	11066	2.23	1.0E-120	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1400	6397	11452	6.07	1.0E-120	N44873.1	EST_HUMAN	y40g12.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:273768 5'
1566	6563	11626	4.73	1.0E-120	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1770	6762	11850	3.83	1.0E-120	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2049	7031	12143	1.03	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2049	7031	12144	1.03	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
3235	6356	10368	0.89	1.0E-120	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
4232	9226	14209	1.43	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4232	9226	14210	1.43	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4527	9517	14503	2.41	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
4527	9517	14504	2.41	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
72	5150	10159	2.65	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
377	5424	10439	1.27	1.0E-121	AU134983.1	EST_HUMAN	AU134983 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
714	7728	10754	1.28	1.0E-121	6032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
2501	7469	12584	1.28	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCI CGAP Bm84 Homo sapiens cDNA clone IMAGE:4150288 5'
2501	7469	12585	1.28	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCI CGAP Bm84 Homo sapiens cDNA clone IMAGE:4150288 5'
2899	7918	12839	0.88	1.0E-121	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit III gene, complete cds; and unknown genes
3007	8024	13036	4.04	1.0E-121	Y19208.1	NT	Homo sapiens HBB3 gene for hair keratin, exons 1 to 9
3007	8024	13037	4.04	1.0E-121	Y19208.1	NT	Homo sapiens HBB3 gene for hair keratin, exons 1 to 9
3459	8467	13494	0.84	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3459	8467	13495	0.84	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3593	8600	13607	8.01	1.0E-121	AF155158.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
4204	9197	14179	1.34	1.0E-121	A1263294.1	EST_HUMAN	q57b01.x1 NCI CGAP_Pent1 Homo sapiens cDNA clone IMAGE:2005417 3'
4817	9801	14781	3.38	1.0E-121	X91937.1	NT	H. sapiens ECE-1 gene (exon 17)
5008	9979	14954	1.26	1.0E-121	AB032481.1	NT	Homo sapiens HOXD13 gene for homeobox transcription factor, complete cds
265	5324	10333	1.82	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
334	5388	10393	3.2	1.0E-122	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
356	5406	10418	1.71	1.0E-122	11526178	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
871	5889	10931	2.93	1.0E-122	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
1200	6201	11238	3.95	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
1854	6850	11722	3.55	1.0E-122	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1874	6870	11746	5.77	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1874	6870	11747	5.77	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1778	6770	11882	4.64	1.0E-122	BE060624.1	EST_HUMAN	601497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899358 5'
2420	7391	12511	20.14	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2420	7391	12512	20.14	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2768	7787	12810	0.98	1.0E-122	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
4699	9884	14667	2.44	1.0E-122	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
4832	9816		1.49	1.0E-122	AW504645.1	EST_HUMAN	U1-HF-BN0-ali-a-03-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079948 5'
759	6780	10807	2.05	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153670 5'
759	6780	10808	2.05	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153670 5'
997	6009	11039	5.43	1.0E-123	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1006	6016	11046	5.48	1.0E-123	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1219	6218	11260	4.18	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1219	6218	11261	4.18	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1428	6425	11484	2.56	1.0E-123	AJ388841.1	NT	Homo sapiens partial mRNA for immunoglobulin kappa chain variable region (IGVK gene), sample GN02
2042	7024	12134	1.75	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2042	7024	12135	1.75	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2042	7024	12136	1.75	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2251	7228		2.82	1.0E-123	7705962	NT	Homo sapiens RAB8-like protein (LOC51209), mRNA
4326	9318		0.93	1.0E-123	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C086
266	5325	10334	2.41	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
266	5325	10335	2.41	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
272	5331		1.29	1.0E-124	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
482	5519	10530	2.33	1.0E-124	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
682	5706	10717	5.13	1.0E-124	AA397551.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
682	5706	10718	5.13	1.0E-124	AA397551.1	EST_HUMAN	z181b04.r1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
749	5771	10788	8.09	1.0E-124	AF155654.1	NT	G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
789	5820	10850	1.42	1.0E-124	4507500	NT	z181b04.r1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
893	5911	10950	2.86	1.0E-124	7705446	NT	G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
1328	6328	11373	4.52	1.0E-124	AF274892.1	NT	Human putative ribosomal protein S1 mRNA
1328	6328	11374	4.52	1.0E-124	AF274892.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1778	6771	11863	4.44	1.0E-124	AJ131712.1	NT	Homo sapiens hypothetical protein (HSPC068), mRNA
							Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
							Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
							Homo sapiens RNA-helicase (rnh61 gene)

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2009	6992	12096	1.32	1.0E-124	BE878524.1	EST_HUMAN	601491715F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893954 5'
2388	7359	12481	1.32	1.0E-124	AB024089.1	NT	Homo sapiens gene for B120, exon 11
3410	8419	13447	0.74	1.0E-124	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3410	8419	13448	0.74	1.0E-124	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3584	8571	13577	1.19	1.0E-124	X13784.1	NT	H. sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and joined CDS)
3804	8807	13813	0.88	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3882	8960	13950	0.81	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4601	9589	14576	2.01	1.0E-124	AB024089.1	NT	Homo sapiens gene for B120, exon 11
4778	9762		1.39	1.0E-124	M18178.1	NT	Human fibronectin gene extra type III repeat (EDII), exon x+1
317	5372		11.96	1.0E-125	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
423	5081	10065	4.13	1.0E-125	BE743922.1	EST_HUMAN	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5'
718	5741	10768	1.85	1.0E-125	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
849	5888	10909	3.29	1.0E-125	AA042813.1	EST_HUMAN	z653c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to
983	5998	11028	1.83	1.0E-125	AL183210.2	NT	gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
1138	8141	11170	1.77	1.0E-125	7662279	NT	Homo sapiens chromosome 21 segment HS21C010
1775	8767	11858	2.36	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
1775	8767	11859	2.36	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
2287	7272	12389	2.15	1.0E-125	AA011278.1	EST_HUMAN	201g09.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429588 5'
2431	7402	12521	1.54	1.0E-125	AA042813.1	EST_HUMAN	z653c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to
2520	7487	12805	1.74	1.0E-125	4504696	NT	gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2520	7487	12806	1.74	1.0E-125	4504696	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
2940	10044	12878	0.98	1.0E-125	BE018009.1	EST_HUMAN	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
3768	8771	13776	2.21	1.0E-125	AA042813.1	EST_HUMAN	601141132F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140786 5'
4419	9409	14396	2.44	1.0E-125	11425114	NT	Homo sapiens CDC-like kinase (CLK) mRNA
4419	9409	14397	2.44	1.0E-125	11425114	NT	Human laminin B1 chain gene, exon 20
4484	9474	14454	1.81	1.0E-125	BE316412.1	EST_HUMAN	H. sapiens gene for alpha1-antichymotrypsin, exon 3
765	5786	10815	1.81	1.0E-126	M61936.1	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
768	5789	10818	2.59	1.0E-126	X68735.1	NT	
808	5925	10860	1.36	1.0E-126	X68735.1	NT	
2283	7259	12377	1.21	1.0E-126	8923056	NT	

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Table 4
Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2283	7259	12378	1.21	1.0E-128	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
2521	7488	12607	2.83	1.0E-126	6382078	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA
2999	8017	13030	54.41	1.0E-126	AA160709.1	EST_HUMAN	zo72c03.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5'
2998	8017	13031	54.41	1.0E-128	AA160709.1	EST_HUMAN	zo72c03.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5'
3545	8552	13559	0.75	1.0E-126	X63941.1	NT	H. sapiens DNA for liver cytochrome b5 pseudogenis
3571	8578	13594	2.04	1.0E-126	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
4842	8627	14619	0.98	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4842	8627	14620	0.98	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4887	8672	14654	1.53	1.0E-126	N34076.1	EST_HUMAN	yx78c06.r1 Soares melanocyte 2NBM Homo sapiens cDNA clone IMAGE:287850 5'
171	5236	10247	8.83	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
171	5236	10248	8.83	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
172	5236	10247	8.4	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
172	5236	10248	8.4	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
271	5330	10342	1.45	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
271	5330	10343	1.45	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
870	5988	10930	1.36	1.0E-127	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
905	5922	10959	1.51	1.0E-127	U72621.2	NT	Homo sapiens lost on transformation LOT1 mRNA, complete cds
1652	6648	11720	1.92	1.0E-127	4827053	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2013	6996	12099	2.09	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2013	6996	12100	2.09	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2137	7117	12231	38.06	1.0E-127	4505620	NT	Homo sapiens ribosomal protein L26 (RPL26) mRNA
2280	7256	12374	2.58	1.0E-127	AF245505.1	NT	Homo sapiens edlican mRNA, complete cds
2535	7500	12820	16.49	1.0E-127	X12881.1	NT	Human mRNA for cytokeratin 18
3606	8613	13621	0.82	1.0E-127	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3721	8725	13725	17.44	1.0E-127	AW161297.1	EST_HUMAN	au80e08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782594 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ;contains element MER22 repetitive element ;
4132	9127	14110	22.49	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4132	9127	14111	22.49	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4472	9462	14441	5.1	1.0E-127	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
4498	9498		3.63	1.0E-127	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C066
4537	9527	14513	1.21	1.0E-127	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
457	6494	10506	4.57	1.0E-128	BE385617.1	EST_HUMAN	601278127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618822 5'
2018	7001	12104	12.08	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2018	7001	12105	12.08	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2147	7126	12243	127.93	1.0E-128	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
2377	7349		4.72	1.0E-128	11437455	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA
3310	8321	13344	1.28	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds
4529	8519	14508	4.83	1.0E-128	11426873	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
122	6447	10469	1.18	1.0E-129	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
410	5447	10469	1.25	1.0E-129	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1680	6678	11750	3.33	1.0E-129	AL098880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
1685	6681	11755	1.56	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1685	6681	11755	1.56	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1809	6789	11890	5.19	1.0E-129	11418522	NT	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA
3055	8072	13082	1.71	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3055	8072	13083	1.71	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3055	8072	13084	1.71	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
4010	9006	13994	1.03	1.0E-129	5032230	NT	Homo sapiens A kinase (PRKA) anchor protein 9 (AKAP9), mRNA
4010	9006	13995	1.03	1.0E-129	5032230	NT	Homo sapiens A kinase (PRKA) anchor protein 9 (AKAP9), mRNA
4040	8036	14026	1.86	1.0E-129	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
4158	9153	14135	2.16	1.0E-129	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151835 similar to CMYA5
4158	9153	14138	2.16	1.0E-129	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151835 similar to CMYA5
75	5153	10163	1.95	1.0E-130	7705530	NT	Cardiomyopathy associated gene 5
1627	6624	11693	31.59	1.0E-130	BE275192.1	EST_HUMAN	Homo sapiens hypothetical protein (HSPC242), mRNA
1627	6624	11694	31.59	1.0E-130	BE275192.1	EST_HUMAN	601121899F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5'
1937	6923		2.05	1.0E-130	X04092.1	NT	Human gene for cathepsin (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13
2698	7655		5.31	1.0E-130	AJ010230.1	NT	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2809	7829	12844	1.17	1.0E-130	BE664219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
2809	7829	12845	1.17	1.0E-130	BE664219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3497	8505	13520	0.78	1.0E-130	AF240698.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3681	7829	12844	5.51	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3681	7829	12845	5.51	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3833	8835	13841	1.54	1.0E-130	AW503580.1	EST_HUMAN	U1-HF-BN0-aky-g-08-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
3960	8988	13947	1.25	1.0E-130	M87710.1	NT	Human T-cell receptor (V alpha 22.1, J alpha RPI)4265-variant, C alpha 1) mRNA
4408	8399	14383	9.21	1.0E-130	AW843983.1	EST_HUMAN	CM4-CN0045-180200-511-402 CN0045 Homo sapiens cDNA
4926	8903	14880	1.3	1.0E-130	AW363298.1	EST_HUMAN	RCO-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
4926	8903	14881	1.3	1.0E-130	AW363298.1	EST_HUMAN	RCO-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
4	5085	10069	1.8	0.0E+00	AA228126.1	EST_HUMAN	z58c04.r1 Soares_NHIMP_u_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G2222811
4	5085	10070	1.8	0.0E+00	AA228126.1	EST_HUMAN	G2222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
8	5088	10074	1.14	0.0E+00	4885136	NT	z58c04.r1 Soares_NHIMP_u_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G2222811
21	5101	10085	5.04	0.0E+00	D83327.1	NT	G2222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
21	5101	10086	5.04	0.0E+00	D83327.1	NT	Homo sapiens checkpoint suppressor 1 (CHES1), mRNA
27	5107	10091	107.34	0.0E+00	AF141349.1	NT	Homo sapiens DCRR1 mRNA, partial cds
35	5115	10101	1.77	0.0E+00	5802997	NT	Homo sapiens beta-tubulin mRNA, complete cds
37	5117	10104	0.74	0.0E+00	M58600.1	NT	Homo sapiens Cdc42 effector protein 2 (CEP2), mRNA
41	5121	10109	24.17	0.0E+00	6957625	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
58	5138	10136	4.3	0.0E+00	Y17151.2	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
58	5138	10137	4.3	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
60	5140	10141	2.89	0.0E+00	D78804.1	EST_HUMAN	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
60	5140	10142	2.89	0.0E+00	D78804.1	EST_HUMAN	HUM516108B Human placenta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-516H08 5'
61	5141	10143	54.73	0.0E+00	L16558.1	NT	HUM516108B Human placenta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-516H08 5'
63	5143	10146	11.31	0.0E+00	AW069534.1	EST_HUMAN	Human ribosomal protein L7 (RPL7) mRNA, complete cds
63	5143	10147	11.31	0.0E+00	AW069534.1	EST_HUMAN	cr48e07.x1 Jla bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07 3'
74	5152	10161	2.95	0.0E+00	4759877	NT	cr48e07.x1 Jla bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07 3'
74	5152	10162	2.95	0.0E+00	4759877	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
77	5152	10161	1.73	0.0E+00	4759877	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
77	5152	10162	1.73	0.0E+00	4759877	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
80	5157	10168	0.7	0.0E+00	4501850	NT	Homo sapiens amiloride binding protein 1 (amine oxidase (copper-containing)) (ABP-1), nuclear gene encoding mitochondrial protein, mRNA
81	5158	10177	50.8	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
90	5167	10177	77.93	0.0E+00	5016088	NT	Homo sapiens actin, beta (ACTB) mRNA
93	5170	10180	45.78	0.0E+00	U89277.1	NT	Human polyhomeotic 1 homolog (HPH1) mRNA, partial cds

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
100	5177	10187	2.36	0.0E+00	AI114743.1	EST_HUMAN	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
101	5178	10188	1.89	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
116	5188	10197	0.91	0.0E+00	AB623701.1	EST_HUMAN	ts38b05.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
117	5188	10197	1.65	0.0E+00	AB623701.1	EST_HUMAN	ts38b05.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
118	7690	10198	3.4	0.0E+00	N36040.1	EST_HUMAN	yy01h09.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270017 5'
118	7690	10199	3.4	0.0E+00	N36040.1	EST_HUMAN	yy01h09.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270017 5'
121	5191	10204	0.7	0.0E+00	4505458	NT	Homo sapiens neuropilin 2 (NRP2) mRNA
131	5197	10212	4.8	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
131	5197	10213	4.8	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
140	5205	10220	1.18	0.0E+00	T56945.1	EST_HUMAN	ya83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
140	5205	10221	1.18	0.0E+00	T56945.1	EST_HUMAN	ya83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
152	5218		70.7	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
158	5222	10234	3.22	0.0E+00	BF036881.1	EST_HUMAN	601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3663803 5'
158	5224		143.39	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
161	5227	10237	0.82	0.0E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
163	5229	10238	6.28	0.0E+00	BE265973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
164	5229	10238	1.45	0.0E+00	BE265973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
165	5230	10239	6.65	0.0E+00	W73973.1	EST_HUMAN	zb62b05.r1 Soares fetal heart NBH19W Homo sapiens cDNA clone IMAGE:345201 5' similar to gb:Y16282 cds1 ZINC FINGER PROTEIN CLONE 947 (HUMAN);
166	5231	10240	2.09	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-404 HT0457 Homo sapiens cDNA
166	5231	10241	2.09	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-404 HT0457 Homo sapiens cDNA
167	5232	10242	3.77	0.0E+00	AF244088.1	NT	Homo sapiens zinc finger protein mRNA, complete cds
170	5235	10245	15.16	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
170	5235	10246	15.16	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
180	5243	10253	9.87	0.0E+00	BE018970.1	EST_HUMAN	bb24a12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z CE22631 ;
180	5243	10254	9.87	0.0E+00	BE018970.1	EST_HUMAN	bb24a12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z CE22631 ;
185	5248	10257	4.23	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
185	5248	10258	4.23	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
186	5249	10259	3.83	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
188	5249	10260	3.83	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds

Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
194	5258	10271	281.78	0.0E+00	D50659.1	NT	Human gamma-cytoplasmic actin (ACTGP9) pseudogene
199	5263	10276	3.01	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
199	5263	10277	3.01	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
201	5265	10278	28.3	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
201	5265	10280	28.3	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
210	7715	10288	57.42	0.0E+00	AI587308.1	EST_HUMAN	ig04f08.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN 1 (HUMAN);
210	7715	10287	57.42	0.0E+00	AI587308.1	EST_HUMAN	ig04f08.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN 1 (HUMAN);
212	5275	10289	1.9	0.0E+00	AF186558.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
214	5277		99.79	0.0E+00	4508632	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
215	5278		15.17	0.0E+00	AF132000.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
220	5283	10293	3.41	0.0E+00	AB018264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
221	5283	10293	3.35	0.0E+00	AB018264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
222	5284	10294	4.92	0.0E+00	6678444	NT	Mus musculus testis-specific protein, Y-encoded-like (Tspyl), mRNA
236	5298	10309	16.43	0.0E+00	5453805	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
238	5300		17.29	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C00.1
245	5305	10315	3.82	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
247	5307	10318	1.5	0.0E+00	X89772.1	NT	H. sapiens mRNA for interferon alpha/beta receptor (long form)
255	5315		6.35	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
267	5326	10336	1.48	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
267	5326	10337	1.48	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
269	5328	10339	2.14	0.0E+00	7706028	NT	Homo sapiens hypothetical protein (LOC51250), mRNA
280	5338		2.81	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
281	5339	10352	2.43	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
281	5339	10353	2.43	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
282	5340		0.88	0.0E+00	AW846293.1	EST_HUMAN	IL2-CT0031-181199-020-B03 CT0031 Homo sapiens cDNA
291	5348	10360	5.4	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 16 (KCNJ16) mRNA
291	5348	10361	5.4	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
302	5359	10371	5.25	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
303	5360	10372	4.98	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
304	7718		48.48	0.0E+00	4508728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
305	5361	10373	2.02	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylmidoimidazole synthetase (GART) mRNA

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
306	5362		2.32	0.0E+00	AA480002.1	EST_HUMAN	z18c08.r1 Soares_NhiMFPu_S1 Homo sapiens cDNA clone IMAGE:753994 5'
307	5363	10374	20.77	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
308	5363	10374	22.16	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
312	5367	10378	2.2	0.0E+00	AF114488.1	NT	Homo sapiens SON DNA binding protein (SON) mRNA, complete cds
325	5379	10387	2.91	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
325	5379	10388	2.91	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
326	5380	10389	3.75	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK) mRNA
327	5380	10389	2.04	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK) mRNA
342	5394	10401	2.33	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
343	5395	10402	1.6	0.0E+00	4505256	NT	Homo sapiens moesin (MSN), mRNA
346	5398	10406	10.77	0.0E+00	4827057	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
349	5401	10411	2.29	0.0E+00	U71600.1	NT	Human zinc finger protein zfp31 (zfp31) mRNA, partial cds
354	5405	10415	2.65	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
354	5405	10416	2.65	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
355	7719	10417	3.33	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
357	5407	10418	1.13	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
360	5410	10423	1.36	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
361	5411	10424	2.25	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
362	5411	10424	1.75	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
364	5413	10426	1.21	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
375	5422	10437	2.21	0.0E+00	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
386	5461	10479	7.9	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
387	5462	10480	7.2	0.0E+00	A136301.4.1	EST_HUMAN	qy61h05.x1 NCI_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2018457 3' similar to gb.X54199
391	5429	10444	3.05	0.0E+00	AW754180.1	EST_HUMAN	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (HUMAN);
394	5431	10447	1.12	0.0E+00	4503680	NT	RC2-CT0320-300100-018-a09 CT0320 Homo sapiens cDNA
395	5432	10448	2.02	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
395	5432	10449	2.02	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
396	5433	10450	1.2	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
397	5434	10451	1.19	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
397	5434	10452	1.19	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
398	5435	10453	3.59	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
399	5436	10454	3.82	0.0E+00	X74870.1	NT	H.sapiens gene for RNA pol II largest subunit, exons 23-28

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
399	5436	10455	3.82	0.0E+00	X74870.1	NT	H.sapiens gene for RNA pol II largest subunit, exons 23-29
400	5436	10454	3.87	0.0E+00	X74870.1	NT	H.sapiens gene for RNA pol II largest subunit, exons 23-29
401	5436	10455	3.87	0.0E+00	X74870.1	NT	H.sapiens gene for RNA pol II largest subunit, exons 23-29
404	5440		114.34	0.0E+00	4506808	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
417	5075	10059	1.06	0.0E+00	R17795.1	EST_HUMAN	y09a02.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31652 5'
425	5463	10481	2.62	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,
426	5464		36.55	0.0E+00	4506728	NT	phosphoribosylmethylimidazole synthetase (GART) mRNA
427	5465	10482	3.49	0.0E+00	AB028942.1	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
428	5466	10483	6.44	0.0E+00	4507152	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
428	5466	10484	6.44	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
429	5467	10485	3.81	0.0E+00	AF193607.1	NT	Homo sapiens SON DNA binding protein (SON) mRNA
441	5478		0.76	0.0E+00	AL163201.2	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds
443	5480	10498	3.88	0.0E+00	4557879	NT	Homo sapiens chromosome 21 segment HS21C001
448	5485		1.31	0.0E+00	AA324262.1	EST_HUMAN	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
449	5486		2.44	0.0E+00	BE254447.1	EST_HUMAN	EST127054 Cerebellum II Homo sapiens cDNA 5' end
465	5502	10512	5.86	0.0E+00	4504532	NT	601111620F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352348 5'
465	5502	10513	5.88	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
470	5506	10520	21.4	0.0E+00	4557887	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
470	5506	10521	21.4	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
480	5517	10527	2.88	0.0E+00	AL163246.2	NT	Homo sapiens keratin 18 (KRT18) mRNA
481	5518	10528	5.35	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
481	5518	10529	5.35	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
480	5526	10534	3.11	0.0E+00	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
492	5528	10536	1.82	0.0E+00	AU132898.1	EST_HUMAN	AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4000837 5'
500	5538	10542	4.41	0.0E+00	BE385144.1	EST_HUMAN	601274951F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3815756 5'
501	7722	10543	4.79	0.0E+00	AW938826.1	EST_HUMAN	PMO-DT0085-130400-002-006 DT0085 Homo sapiens cDNA
504	5539	10545	1.51	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
505	5540	10546	0.81	0.0E+00	8923955	NT	Homo sapiens PC326 protein (PC326), mRNA
508	5543		0.68	0.0E+00	BF373403.1	EST_HUMAN	IL2-FT0159-070800-120-F07 FT0159 Homo sapiens cDNA
515	5550	10555	4.2	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
522	7723	10559	1.9	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-H05 BT0635 Homo sapiens cDNA
527	5562	10565	1.86	0.0E+00	BF028005.1	EST_HUMAN	601764858F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3966998 5'
532	5567	10570	1.25	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
535	5570	10573	17.58	0.0E+00	6006030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
536	5571	10574	5.39	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
536	5571	10575	5.39	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
538	5573	10577	3.44	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
539	5574	10578	2.68	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
539	5574	10579	2.68	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
544	5578		3.9	0.0E+00	AF003528.1	NT	Homo sapiens X-linked arthralgia ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
552	5588	10588	1.35	0.0E+00	AW135324.1	EST_HUMAN	UI-H-B1-acb-h-04-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2713951 3'
561	5595		4.5	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
581	5613	10613	7.89	0.0E+00	5174742	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRCF1), nuclear gene encoding mitochondrial protein, mRNA
584	5625		4.24	0.0E+00	J04066.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1
597	5628	10627	2.06	0.0E+00	BF104898.1	EST_HUMAN	601822827F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045447 5'
599	5630	10629	1.05	0.0E+00	8923831	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
599	5630	10630	1.05	0.0E+00	8923831	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
600	5630	10629	0.82	0.0E+00	8923831	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
600	5630	10630	0.82	0.0E+00	8923831	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
601	5630	10629	0.7	0.0E+00	8923831	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
601	5630	10630	0.7	0.0E+00	8923831	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
610	5637	10638	0.83	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
610	5637	10639	0.83	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
617	5644	10646	2.81	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
619	5646	10649	2.39	0.0E+00	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
621	5648	10650	0.76	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
622	5649	10651	1.52	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
622	5649	10652	1.52	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
628	5657	10662	2.63	0.0E+00	AA399486.1	EST_HUMAN	z660c07.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:726732 5'
633	5661	10666	6.46	0.0E+00	D11078.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
638	5666		3.25	0.0E+00	4985526	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
645	5673	10678	2.37	0.0E+00	6006003	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
647	5675	10681	2.08	0.0E+00	5031824	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
650	5678	10685	3.14	0.0E+00	U05235.1	NT	Human neutral amino acid transporter (ASCT1) gene, exon 8
654	5682	10688	1.1	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
654	5682	10689	1.1	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
660	5687	10694	4.21	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
660	5687	10695	4.21	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
666	7726		1.79	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV8)
674	5699	10708	21.88	0.0E+00	4504424	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 1 (HMG1) mRNA
678	5703	10711	15.74	0.0E+00	AB028012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
688	5712	10728	6.92	0.0E+00	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
699	5723	10739	47.96	0.0E+00	AA614537.1	EST_HUMAN	np49d01.s1 NCI CGAP_Br1.1 Homo sapiens cDNA clone IMAGE:1129633 3' similar to gb:X57352
703	5727	10743	4.04	0.0E+00	M60875.1	NT	INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN);
703	5727	10744	4.04	0.0E+00	M60875.1	NT	Human von Willebrand factor gene, exons 23 through 34
713	5737	10753	1.32	0.0E+00	5032192	NT	Human von Willebrand factor gene, exons 23 through 34
719	5742	10759	3.44	0.0E+00	AF264750.1	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
719	5742	10760	3.44	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
721	5744	10763	11.53	0.0E+00	11545800	NT	Homo sapiens ALR-like protein mRNA, partial cds
727	5750	10771	2.72	0.0E+00	BE241577.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
747	5769	10795	1.78	0.0E+00	AF226990.2	NT	TCAAP1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0779
747	5769	10796	1.78	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
750	5772	10799	3.03	0.0E+00	J03764.1	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
750	5772	10800	3.03	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
752	5774	10801	1.73	0.0E+00	AB037760.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
753	5775	10802	1.35	0.0E+00	6912749	NT	Homo sapiens mRNA for KIAA1339 protein, partial cds
755	7730	10804	4.57	0.0E+00	D30812.1	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
756	5777	10805	5.14	0.0E+00	BE869735.1	EST_HUMAN	Homo sapiens mRNA for repressor protein, partial cds
760	5781	10809	3.82	0.0E+00	R48915.1	EST_HUMAN	Homo sapiens mRNA for repressor protein, partial cds
761	5782	10810	5.54	0.0E+00	5032086	NT	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
770	5791	10819	1.61	0.0E+00	AB011399.1	NT	y68908.r1 Soares breast 2NHBst Homo sapiens cDNA clone IMAGE:154048 5'
773	5795	10823	3.45	0.0E+00	7661985	NT	Homo sapiens splicing factor 3a, subunit 1, 120kD (SF3A1), mRNA
784	5805	10835	1.58	0.0E+00	D80006.1	NT	Homo sapiens gene for AF-6, complete cds
784	5805	10836	1.58	0.0E+00	D80006.1	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
789	5810	10840	2.89	0.0E+00	X89772.1	NT	Human mRNA for KIAA0184 gene, partial cds
793	5814	10844	3.13	0.0E+00	AB020717.1	NT	Human mRNA for KIAA0184 gene, partial cds
793	5814	10845	3.13	0.0E+00	AB020717.1	NT	H. sapiens mRNA for interferon alpha/beta receptor (long form)
793	5814	10846	3.13	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
793	5814	10846	3.13	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
797	5818	10848	10.62	0.0E+00	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
798	5819		8.45	0.0E+00	4607500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
814	5835	10870	1.57	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
815	5836	10871	2.15	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
817	5838	10873	1.84	0.0E+00	4557688	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KCNE1) mRNA
823	5843	10879	1.98	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
823	5843	10880	1.98	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
824	5844	10881	1.05	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
826	5849	10886	1.72	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
833	5852	10891	2.11	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
833	5852	10892	2.11	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
840	5859		1.37	0.0E+00	AF027163.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds
844	5863	10903	4.35	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
844	5863	10904	4.35	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
845	5864	10905	11.54	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
846	5865	10906	4.49	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
847	5866	10907	28.07	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
850	5869	10910	1.1	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
850	5869	10911	1.1	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
851	5870	10912	1.78	0.0E+00	AA533272.1	EST_HUMAN	U66d07.s1 NCI_CGAP_P10 Homo sapiens cDNA, clone IMAGE:397453
851	5870	10913	1.78	0.0E+00	AA533272.1	EST_HUMAN	U66d07.s1 NCI_CGAP_P10 Homo sapiens cDNA, clone IMAGE:397453
852	5871		6.52	0.0E+00	BF877694.1	EST_HUMAN	602085578F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
856	5875	10914	1.36	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
856	5875	10915	1.36	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
857	5876	10916	2.29	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
857	5876	10917	2.29	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
880	5898	10940	1.27	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
887	5905	10945	1.4	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
887	5905	10946	1.4	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
897	5915	10955	2.23	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
907	5924		92.58	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
910	5924		105.51	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
911	5927	10962	1.55	0.0E+00	AF089747.1	NT	Homo sapiens alpha-1-antichymotrypsin precursor, mRNA, partial cds
912	5928	10963	1.39	0.0E+00	L28101.1	NT	Homo sapiens kallistatin (P14) gene, exons 1-4, complete cds

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
936	5953	10985	1.21	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
937	5954	10986	6.98	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
938	5955	10987	0.78	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
939	5956	10988	1.55	0.0E+00	4507430	NT	Homo sapiens thymidine phosphorylase (TEF), mRNA
939	5956	10989	1.55	0.0E+00	4507430	NT	Homo sapiens thymidine phosphorylase (TEF), mRNA
947	7735	10996	1.94	0.0E+00	AI001948.1	EST_HUMAN	os98e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
947	7735	10997	1.94	0.0E+00	AI001948.1	EST_HUMAN	os98e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
949	5965	10999	7.69	0.0E+00	7657266	NT	Homo sapiens KIAA0929 protein Mix2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
960	5975	11009	1.89	0.0E+00	AB030566.1	NT	Homo sapiens mRNA for PSP24, complete cds
968	5983	11015	1.14	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
968	5983	11016	1.14	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
968	5983	11017	1.14	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
969	5984	11018	1.55	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
969	5984	11019	1.55	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
978	5993	11026	2.93	0.0E+00	4757899	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL), mRNA
989	6003	11034	3.09	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
990	6004	11035	58.93	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
991	6004	11035	27.22	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
994	6007		5.92	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
995	6007		11.99	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
998	6010	11040	1.12	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
999	6010	11040	1.89	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1000	6010	11040	1.74	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1001	6011	11041	6.04	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1004	6014	11044	2.82	0.0E+00	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1008	6018	11048	4.81	0.0E+00	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (IMMT), mRNA
1009	6019		4.43	0.0E+00	AA459680.1	EST_HUMAN	aa86g07.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838236 3' similar to SW:PRS8_HUMAN P47210 26S PROTEINASE REGULATORY SUBUNIT 8 ;
1012	6022	11052	0.8	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1012	6022	11053	0.8	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1013	6023	11054	1.08	0.0E+00	4758249	NT	Homo sapiens TRAF family member-associated NIKB activator (TANK), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1013	6023	11055	1.08	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1016	6026		5.63	0.0E+00	8922933	NT	Homo sapiens hypothetical protein FLJ11198 (FLJ11198), mRNA
1030	6040	11070	10	0.0E+00	4758569	NT	Homo sapiens heat shock 70kD protein 98 (hsc70) (HSPA9B) mRNA
1048	6057	11085	3.04	0.0E+00	4826872	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1048	6057	11088	3.04	0.0E+00	4826872	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1052	6061	11090	3.88	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1052	6061	11091	3.88	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1053	6082	11092	127.96	0.0E+00	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1055	6084		1.04	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1057	6066	11088	4.28	0.0E+00	6174384	NT	Homo sapiens alkylation repair, alkB homolog (ABH), mRNA
1066	6074	11107	3.16	0.0E+00	4758117	NT	Homo sapiens Death associated protein 3 (DAP3) mRNA
1079	6086	11115	5.78	0.0E+00	BE005208.1	EST_HUMAN	MRO-BN0115-200300-003-h08 BN0115 Homo sapiens cDNA
1102	6109	11139	4.27	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1102	6109	11140	4.27	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1115	6121	11150	1.67	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1115	6121	11151	1.67	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1116	6122	11152	46.69	0.0E+00	4506712	NT	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1118	6124	11154	2.22	0.0E+00	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1121	6127	11157	37.23	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1123	6129	11158	82.18	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1124	6130	11159	4.76	0.0E+00	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1124	6130	11160	4.76	0.0E+00	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1127	6132	11162	4.36	0.0E+00	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
1128	6133	11163	0.66	0.0E+00	X95828.1	NT	H. sapiens ART4 gene
1128	6133	11164	0.66	0.0E+00	X95828.1	NT	H. sapiens ART4 gene
1129	6134	11165	1.23	0.0E+00	A1147650.1	EST_HUMAN	qb22d10.x1 Soares_pregnan_ uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697011 3'
1131	6136	11167	3.05	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1138	6143	11173	0.86	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1138	6143	11174	0.86	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1139	6144	11175	1.05	0.0E+00	996844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
1150	6154	11186	5.48	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1150	6154	11187	5.48	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1152	6156	11189	0.98	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1159	6163	11188	14.52	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1172	6175	11209	1.01	0.0E+00	AF073299.1	NT	Homo sapiens Na ⁺ /H ⁺ exchanger isoform 2 (NHE2) mRNA, complete cds
1180	6181		1.32	0.0E+00	7657336	NT	Homo sapiens mut. (E. coli) homolog 3 (MLH3), mRNA
1203	6204	11241	0.69	0.0E+00	8922593	NT	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA
1206	6207	11244	0.89	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1208	6207	11245	0.89	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1207	6208	11246	1.55	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1208	7741	11247	1.09	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1227	6226	11272	4.89	0.0E+00	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1228	6227	11273	2.52	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1238	6236	11278	4.31	0.0E+00	4505740	NT	Homo sapiens profilin 4 (PFND4) mRNA
1247	6245		2.72	0.0E+00	Y18000.1	NT	Homo sapiens NF2 gene
1255	6253	11294	283.18	0.0E+00	4508718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1262	6260	11303	5.64	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSOR9) mRNA, complete cds
1268	6268	11307	1.42	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1268	6266	11308	1.42	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1281	6280	11321	2.45	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1281	6280	11322	2.45	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1281	6280	11323	2.45	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1282	6281		2.35	0.0E+00	AF086156.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 5
1292	7743	11335	1.18	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1292	7743	11336	1.16	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1296	6294	11341	1.37	0.0E+00	5803146	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1297	6295	11342	2.28	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1299	6297	11343	0.67	0.0E+00	5803146	NT	Homo sapiens zinc finger protein 9 (RNF9), mRNA
1300	6298	11344	2.07	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1302	6300	11346	4.17	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1303	6301	11347	9.28	0.0E+00	7661865	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1304	6302	11348	10.18	0.0E+00	7661865	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1305	6303	11349	3.67	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1305	6303	11350	3.67	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1317	6314	11363	1.22	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
1376	6372	11421	1.64	0.0E+00	BE257855.1	EST_HUMAN	601109792F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350471 5'
1376	6372	11422	1.64	0.0E+00	BE257855.1	EST_HUMAN	601109792F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350471 5'
1384	6381	11431	1.51	0.0E+00	AJ250014.1	NT	Homo sapiens mRNA for Familial Cylindromatosis c1d gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit: Descriptor
1392	6388	11442	1.16	0.0E+00	A1208756.1	EST_HUMAN	qg38b06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837427 3' similar to WP:T27A1.5 CE14213 ;
1393	6390	11443	28.34	0.0E+00	6042206	NT	RAN, member RAS oncogene familyHomo sapiens RAN, member RAS oncogene family (RAN), mRNA
1401	6398	11453	1.69	0.0E+00	4505846	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1401	6398	11454	1.59	0.0E+00	4505846	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1403	6400	11457	3.9	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1403	6400	11458	3.9	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1405	6402	11459	4.32	0.0E+00	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1413	6411	11470	3.56	0.0E+00	AF038280.1	NT	Homo sapiens alpha1-fucosyltransferase (alpha1-6FucT) gene, exon 7
1434	6431	11487	2.12	0.0E+00	AL132999.1	NT	Novel human gene on chromosome 20
1435	6432	11488	1.3	0.0E+00	AL137764.1	NT	Novel human gene mapping to chromosome 1
1439	6436	11493	1.89	0.0E+00	D87077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1442	6439	11496	6.31	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1444	6441	11498	2.08	0.0E+00	7681985	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1444	6441	11499	2.08	0.0E+00	7681985	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1480	6477	11533	3.1	0.0E+00	7706434	NT	Homo sapiens hHDC for homolog of Drosophila headcase (LOC51696), mRNA
1493	6491	11546	0.99	0.0E+00	AW959687.1	EST_HUMAN	EST371757 MAGE resequences, MAGF Homo sapiens cDNA
1494	6492	11547	2.89	0.0E+00	AA481172.1	EST_HUMAN	aa34a03.r1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815116 5'
1500	6498	11551	42.31	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1500	6498	11552	42.31	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1502	6500	11556	1.1	0.0E+00	AW976097.1	EST_HUMAN	EST388206 MAGE resequences, MAGN Homo sapiens cDNA
1502	6500	11556	1.1	0.0E+00	AW976097.1	EST_HUMAN	EST388206 MAGE resequences, MAGN Homo sapiens cDNA
1503	6501	11557	1.11	0.0E+00	D10884.1	NT	Bovine mRNA for neurocalcin
1505	6503		1.87	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
1508	6504	11560	2.02	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1508	6504	11561	2.02	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1507	6505	11562	2.55	0.0E+00	7692405	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
1508	6506		7.44	0.0E+00	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1513	6511	11568	3	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1516	6514	11570	1.08	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1516	6514	11571	1.08	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1517	7749		39.26	0.0E+00	4508654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1518	6515	11572	61.77	0.0E+00	M14199.1	NT	Human laminin receptor (2H5 epitope) mRNA, 5' end
1530	6528	11587	8.55	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1537	6535		1.85	0.0E+00	D00333.1	NT	human c-yes-2 gene
1545	6543	11601	26.28	0.0E+00	Z83738.1	NT	H. sapiens hH2B/e gene
1546	6544	11602	2.84	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1546	6544	11603	2.84	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1547	6545	11604	6.07	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5'
1547	6545	11605	6.07	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5'
1549	7760	11608	1.72	0.0E+00	AB040905.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1553	6550	11609	2.77	0.0E+00	AF157478.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1555	6552	11612	6.44	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1555	6552	11613	6.44	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1557	6554	11614	84.9	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1557	6554	11615	84.9	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1559	6556	11617	2.3	0.0E+00	M91803.1	NT	Human sodium channel mRNA
1572	6569	11631	9.88	0.0E+00	H26973.1	EST_HUMAN	ye76c05.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:183848 3'
1579	6576	11639	1.95	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1579	6576	11640	1.95	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1598	6594	11655	4.22	0.0E+00	AW444637.1	EST_HUMAN	UI-H-B13-ajw-c-04-Q-UJ.s1 NCJ CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'
1625	6622	11690	8.38	0.0E+00	BE144394.1	EST_HUMAN	MRO-HT0166-191199-004-b11 HT0166 Homo sapiens cDNA
1625	6622	11691	8.38	0.0E+00	BE144394.1	EST_HUMAN	MRO-HT0166-191199-004-b11 HT0166 Homo sapiens cDNA
1629	6626	11695	3.34	0.0E+00	A1768104.1	EST_HUMAN	wg81b07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR:Q62788 Q62788 CYS2HIS2 ZINC FINGER PROTEIN. ;
1630	6627	11696	1.18	0.0E+00	4758513	NT	Homo sapiens hematopoietic-derived zinc finger protein (HD-ZNF1) mRNA
1631	6628	11697	2.39	0.0E+00	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1634	6631	11700	2.07	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1634	6631	11701	2.07	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1636	6633	11703	26.94	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1637	6634	11704	1.45	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
1641	6638	11707	2.18	0.0E+00	BE222374.1	EST_HUMAN	hu11405.x1 NCJ CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O95147 O95147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1641	6638	11708	2.18	0.0E+00	BE222374.1	EST_HUMAN	hu11405.x1 NCJ CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O95147 O95147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1643	6639	11710	1.29	0.0E+00	4557610	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1646	6642	11713	8.67	0.0E+00	H30132.1	EST_HUMAN	yc59e08.r1 Soares breast 3NbHBst Homo sapiens cDNA IMAGE:182246 5' similar to gb:M64089 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1646	6642	11714	8.67	0.0E+00	H30132.1	EST_HUMAN	yc59e08.r1 Soares breast 3NbHBst Homo sapiens cDNA IMAGE:182246 5' similar to gb:M64089 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1648	6644	11716	19.26	0.0E+00	Z80780.1	NT	H.sapiens H2B/h gene
1648	6644	11717	19.26	0.0E+00	Z80780.1	NT	H.sapiens H2B/h gene
1651	6647		64.76	0.0E+00	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1680	6656	11730	5.23	0.0E+00	8923841	NT	Homo sapiens FOXJ2 forkhead factor (LOC55810), mRNA
1683	6659	11733	1.85	0.0E+00	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
1689	6685	11741	1.1	0.0E+00	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMY1A1) mRNA
1675	6671	11748	7.62	0.0E+00	AB028542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
1677	6673		1.82	0.0E+00	S94400.1	NT	TCR zeta [human, Genomic] mRNA, 385 nt, segment 1 of 8
1686	6682	11757	1.82	0.0E+00	4557538	NT	Homo sapiens solute carrier family 26 (sulfate transporter), member 2 (SLC26A2) mRNA
1693	7753	11764	1.05	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
1706	6701	11778	2.59	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1747	7754		150.84	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1752	6746	11826	3.32	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1752	6746	11827	3.32	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1755	6748	11831	2.75	0.0E+00	U63963.1	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1759	7755	11836	8.02	0.0E+00	4505332	NT	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA
1771	6763	11851	22.06	0.0E+00	U14987.1	NT	Human ribosomal protein L21 mRNA, complete cds
1773	6765	11854	12.68	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
1774	6766	11855	13.86	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1774	6766	11856	13.86	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1774	6766	11857	13.86	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1788	6780	11872	1.29	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1788	6780	11873	1.29	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1798	6789	11878	5.58	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1798	6789	11879	5.58	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1807	6788	11888	3.27	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1807	6788	11889	3.27	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1811	6801	11891	3.31	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1811	6801	11892	3.31	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1812	6802	11893	8.06	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1812	6802	11894	8.06	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1815	6805	11897	1.53	0.0E+00	AW207280.1	EST_HUMAN	UI-H-B11-afn-f07-q-J1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1815	6805	11898	1.53	0.0E+00	AW207280.1	EST_HUMAN	UI-H-B11-afn-f07-q-J1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1837	6827	11915	2.87	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1837	6827	11916	2.87	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1878	6867	11955	1.79	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1878	6867	11956	1.79	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1881	6870	11958	2.53	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1881	6870	11959	2.53	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1888	6877	11967	1.87	0.0E+00	AB037788.1	NT	Homo sapiens mRNA for KIAA1367 protein, partial cds
1891	6880		1.55	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1892	7758	11970	1.49	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1892	7758	11971	1.49	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1897	6885	11978	1.31	0.0E+00	4507484	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1897	6885	11979	1.31	0.0E+00	4507484	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1900	6887	11981	1.17	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
1902	6889		6.49	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1907	6894		3.82	0.0E+00	M55632.1	NT	Human topoisomerase I pseudogene 1
1908	7759	11988	1.74	0.0E+00	5901805	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
1910	6898	11990	4.05	0.0E+00	BE018068.1	EST_HUMAN	bb73f1.1.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048045 5'
1916	6902	11995	1.47	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1916	6902	11996	1.47	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1926	6912	12007	9.5	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1926	6912	12008	9.5	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1940	6926	12023	1.41	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
1940	6926	12024	1.41	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
1942	6928	12025	1.95	0.0E+00	AW193024.1	EST_HUMAN	x69b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679913 3'
1942	6928	12026	1.95	0.0E+00	AW193024.1	EST_HUMAN	x69b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679913 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1943	6929	12027	8.45	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1943	6929	12028	8.45	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1945	6931	12030	1.25	0.0E+00	7682095	NT	Homo sapiens KIAA0408 gene product (KIAA0408), mRNA
1946	6932	12031	1.88	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1947	6933	12032	1.43	0.0E+00	Z47556.1	NT	H. sapiens genes for semenogelin I and semenogelin II
1947	6933	12033	1.43	0.0E+00	Z47556.1	NT	H. sapiens genes for semenogelin I and semenogelin II
1954	6940	12042	3.49	0.0E+00	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
1971	6956	12060	0.94	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1971	6956	12061	0.94	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2000	6983	12087	1.1	0.0E+00	7706742	NT	Homo sapiens TP53TG3a (TP53TG3a), mRNA
2004	6987	12091	13.6	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2004	6987	12092	13.6	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2008	6989	12093	1.99	0.0E+00	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2007	6990	12094	1.02	0.0E+00	BF207688.1	EST_HUMAN	601861974F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081483 5'
2008	6991	12095	5.35	0.0E+00	AU140831.1	EST_HUMAN	AU140831 PLACE4 Homo sapiens cDNA clone PLACE4000321 5'
2010	6993	12097	1.29	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library/Homo sapiens cDNA clone 7B22E10
2010	6993	12098	1.29	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library/Homo sapiens cDNA clone 7B22E10
2012	6995		2.47	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2014	6997		1.21	0.0E+00	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2015	6998	12101	1.05	0.0E+00	Z42399.1	EST_HUMAN	HSC01C021 normalized infant brain cDNA Homo sapiens cDNA clone c-01c02
2017	7000		1.43	0.0E+00	AI244247.1	EST_HUMAN	qv90708.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:1988971 3' similar to contains Alu repetitive element;
2021	7004	12109	6.29	0.0E+00	BE877225.1	EST_HUMAN	601485146F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3887747 5'
2023	7006	12111	4.71	0.0E+00	BF315325.1	EST_HUMAN	601902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2023	7006	12112	4.71	0.0E+00	BF315325.1	EST_HUMAN	601902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2028	7011	12118	2.79	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2028	7011	12119	2.79	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2033	7016	12125	2.04	0.0E+00	L00820.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2033	7016	12126	2.04	0.0E+00	L00820.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2036	7019	12129	1.7	0.0E+00	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2055	7037		2.76	0.0E+00	BE767964.1	EST_HUMAN	QV1-GN0065-140900-318-c10 GN0065 Homo sapiens cDNA
2056	7038		1.41	0.0E+00	AF018963.1	NT	Homo sapiens X-linked juvenile retinoschisis protein (XLR51) gene, exon 6 and complete cds
2058	7040	12149	4.46	0.0E+00	BF027582.1	EST_HUMAN	601672066F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2059	7041	12150	1.77	0.0E+00	BE072624.1	EST_HUMAN	PMO-BT0547-210300-004-F04 BT0547 Homo sapiens cDNA
2061	7043	12151	2.11	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2062	7044	12152	3.64	0.0E+00	AW752708.1	EST_HUMAN	IL3-CT0219-271099-022-G10 CT0219 Homo sapiens cDNA
2064	7046	12154	4.62	0.0E+00	AI904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2064	7046	12155	4.62	0.0E+00	AI904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2116	7086		1.21	0.0E+00	L14787.1	NT	Human DNA-binding protein mRNA, 3' end
2122	7102	12214	1.93	0.0E+00	BE274696.1	EST_HUMAN	601122338F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346688 5'
2124	7104	12217	1.01	0.0E+00	DB7685.1	NT	Human mRNA for KIAA0244 gene, partial cds
2125	7105	12218	42.14	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2125	7105	12219	42.14	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2127	7107	12221	3.7	0.0E+00	AA831691.1	EST_HUMAN	cc32e01.s1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1567896 3'
2129	7109		1.02	0.0E+00	M19828.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 22 through 29
2132	7112	12226	52.74	0.0E+00	BF344434.1	EST_HUMAN	602014829F1 NCI CGAP Bnt64 Homo sapiens cDNA clone IMAGE:4150734 5'
2133	7113	12228	55.46	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
2136	7116	12229	4.45	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA
2136	7116	12230	4.45	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA
2140	7164	12235	4.41	0.0E+00	BF313617.1	EST_HUMAN	601900281F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128622 5'
2143	7122	12238	2.4	0.0E+00	BE018750.1	EST_HUMAN	bb84e02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR SII-RELATED PROTEIN ;
2145	7124	12240	2.17	0.0E+00	AA042813.1	EST_HUMAN	zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857 cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2145	7124	12241	2.17	0.0E+00	AA042813.1	EST_HUMAN	zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857 cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2153	7132	12249	2.88	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C00.4
2153	7132	12250	2.86	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C00.4
2154	7133	12251	2.34	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2154	7133	12252	2.34	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2159	7138		2.31	0.0E+00	U36294.1	NT	Human beta-prime-adaplin (BAM22) gene, exon 16
2160	7139	12257	1.43	0.0E+00	AA282281.1	EST_HUMAN	z112510.t1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:712891 5'
2167	7146	12263	2.22	0.0E+00	BE897487.1	EST_HUMAN	601432317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5'
2180	7159	12278	8.49	0.0E+00	4557566	NT	Homo sapiens E1A binding protein p300 (EP300) tRNA
2185	7164	12284	1.93	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2191	7170	12281	6.09	0.0E+00	BE895281.1	EST_HUMAN	601433525F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918607 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2195	7174	12285	2.37	0.0E+00	BE805553.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2195	7174	12286	2.37	0.0E+00	BE805553.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2197	7175	12288	3.61	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
2237	7214	12331	3.28	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 8 (DEF8), mRNA
2237	7214	12332	3.28	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 8 (DEF8), mRNA
2238	7215	12333	2.27	0.0E+00	AI076404.1	EST_HUMAN	ox09c07.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1874828 3'
2241	7218	12336	3.84	0.0E+00	AA428001.1	EST_HUMAN	z178a11.1 Soares_fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:769740 5'
2241	7218	12337	3.84	0.0E+00	AA428001.1	EST_HUMAN	z178a11.1 Soares_fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:769740 5'
2243	7220	12339	3.72	0.0E+00	BF347039.1	EST_HUMAN	602021846F1 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4157339 5'
2248	7225	12345	1.02	0.0E+00	6325496	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2255	7232	12351	2.79	0.0E+00	BE876095.1	EST_HUMAN	7f22a02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3295370 3' similar to TR:O94839 O94839 KIAA0857 PROTEIN ;
2258	7235	12353	18.03	0.0E+00	AF044571.1	NT	Homo sapiens phosphatase kinase alpha subunit (PHKA2) gene, exon 32
2259	7236	12354	1.78	0.0E+00	AI625542.1	EST_HUMAN	y57c08.x1 NCI_CGAP_UJ2 Homo sapiens cDNA clone IMAGE:2283182 3'
2261	7238	12355	1.15	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2264	7241	12357	3.07	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2264	7241	12358	3.07	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2267	7244	12361	3.48	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2267	7244	12362	3.48	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2273	7249	12365	2.22	0.0E+00	7682007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2273	7249	12366	2.22	0.0E+00	7682007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2277	7253	12371	1.4	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2277	7253	12372	1.4	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2287	7263	12380	2.25	0.0E+00	5174678	NT	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA
2291	7266	12384	3.96	0.0E+00	AU131142.1	EST_HUMAN	AU131142 NT2RP3 Homo sapiens cDNA clone NT2RP3002064 5'
2292	7287	12384	47.81	0.0E+00	BE794026.1	EST_HUMAN	601688843F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3941003 5'
2293	7288	12385	2.44	0.0E+00	AW867076.1	EST_HUMAN	MR1-SN0033-120-000-002-a04 SN0033 Homo sapiens cDNA
2294	7269	12386	4.95	0.0E+00	7682017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2295	7270	12387	2.03	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2295	7270	12388	2.03	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2296	7271		4.1	0.0E+00	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2298	7273	12390	21.5	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2298	7273	12391	21.5	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2298	7273	12392	21.5	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2299	7274	12393	1.24	0.0E+00	89233089	NT	Homo sapiens hypothetical protein FLJ20081 (FLJ20081), mRNA
2316	7281		1.51	0.0E+00	BE814424.1	EST_HUMAN	MRO-BN0070-090600-029-d12 BN0070 Homo sapiens cDNA
2348	7322	12441	0.99	0.0E+00	AU119582.1	EST_HUMAN	AU119582 HEMBA1 Homo sapiens cDNA clone HEMBA1006155 5'
2349	7323						ox60b02.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1660683 3' similar to TR:O08662
2350	7324	12442	3.28	0.0E+00	A042035.1	EST_HUMAN	O08662 230KDA PHOSPHATIDYLINOSITOL 4-KINASE. ;
2354	7328		1.18	0.0E+00	8923620	NT	Homo sapiens hypothetical protein FLJ20683 (FLJ20683), mRNA
2365	7339		4.15	0.0E+00	BE895605.1	EST_HUMAN	601432608F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918188 5'
2369	7342	12460	3.39	0.0E+00	AB005622.1	EST_HUMAN	AB005622 Hela cDNA (T.Noma) Homo sapiens cDNA similar to adenylate kinase isozyme 2
2372	7344	12463	5.53	0.0E+00	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
2372	7344	12463	1.57	0.0E+00	D85608.1	NT	Homo sapiens gene for cholestyrolin type-A receptor, complete cds
2372	7344	12464	1.57	0.0E+00	D85608.1	NT	Homo sapiens gene for cholestyrolin type-A receptor, complete cds
2380	7352	12473	1.34	0.0E+00	AF106275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2384	7355	12477	0.95	0.0E+00	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4153670 5'
2390	7361	12484	6.99	0.0E+00	5729777	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2398	7369	12490	16.53	0.0E+00	BF569144.1	EST_HUMAN	602184558F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300383 3'
2407	7378	12497	2.46	0.0E+00	AW468922.1	EST_HUMAN	ha04h04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872789 3'
2409	7380	12498	2.09	0.0E+00	AW501010.1	EST_HUMAN	UI-HF-BP0p-als-c-07-0-UI-1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2433	7404		2.13	0.0E+00	AW813853.1	EST_HUMAN	RC3-ST0197-300300-018-c04 ST0197 Homo sapiens cDNA
2438	7409	12526	27.9	0.0E+00	BE789542.1	EST_HUMAN	601592530F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3948518 5'
2439	6887	11981	1.18	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
2440	7410	12527	1.33	0.0E+00	BF509482.1	EST_HUMAN	UI-H-B14-aoz-b-08-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086535 3'
2443	7413	12529	3.32	0.0E+00	Z32884.2	NT	Homo sapiens mRNA for membrane transport protein (XK gene)
2445	7415		3.21	0.0E+00	5453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFR) mRNA
2448	7418	12533	1.05	0.0E+00	BE910378.1	EST_HUMAN	601503356F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3905148 5'
2449	7419	12534	2.35	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2450	7420	12535	0.91	0.0E+00	BE150865.1	EST_HUMAN	RC4-HT0276-160200-013-d05 HT0276 Homo sapiens cDNA
2451	7421	12536	3.02	0.0E+00	U83239.1	NT	Human Sec62 (Sec62) mRNA, complete cds
2457	7427	12542	2.2	0.0E+00	BE889480.1	EST_HUMAN	601508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909866 5'
2461	7430	12547	4.05	0.0E+00	BE875511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2461	7430	12548	4.05	0.0E+00	BE875511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2462	7431	12549	1.27	0.0E+00	AF114027.1	EST_HUMAN	AF114027 Homo sapiens lung fetus Homo sapiens cDNA clone ESF6
2464	7433	12552	1	0.0E+00	AF245505.1	NT	Homo sapiens adipican mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2480	7449	12560	1.91	0.0E+00	BE536921.1	EST_HUMAN	601084738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5'
2485	7453	12567	3.77	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2485	7453	12568	3.77	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2486	7454	12569	3.86	0.0E+00	BE282886.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887955 5'
2488	7454	12570	3.86	0.0E+00	BE282886.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887955 5'
2487	7455	12571	0.93	0.0E+00	BF223041.1	EST_HUMAN	7927h12.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE: 3' similar to TR:O00246 O00246
2490	7458	12573	5.98	0.0E+00	AF245505.1	NT	HYPOTHETICAL 9.3 KD PROTEIN ;
2508	7476	12591	0.91	0.0E+00	BE296613.1	EST_HUMAN	Homo sapiens edican mRNA, complete cds
2522	7708	12608	1.49	0.0E+00	AB037836.1	NT	601173631F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529159 5'
2522	7708	12609	1.49	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2523	7489	12609	1.95	0.0E+00	BF513835.1	EST_HUMAN	Homo sapiens mRNA for KIAA1415 protein, partial cds
2528	7494	12614	1.25	0.0E+00	BF672818.1	EST_HUMAN	UI-H-BW1-amp-F-12-0-J1.s1 NCL_CGAP_Sub77 Homo sapiens cDNA clone IMAGE:3070631 3'
2530	7496	12614	1.1	0.0E+00	BE616695.1	EST_HUMAN	602182683F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283612 5'
2539	7504	12623	2.22	0.0E+00	AB037742.1	NT	601279873F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3621786 5'
2540	7505	12624	2.36	0.0E+00	5032150	NT	Homo sapiens mRNA for KIAA1321 protein, partial cds
2542	7507	12628	5.08	0.0E+00	AB037859.1	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28kD (TAF2I) mRNA
2543	7508	12627	1.42	0.0E+00	BE795445.1	EST_HUMAN	Homo sapiens mRNA for KIAA1438 protein, partial cds
2543	7508	12628	1.42	0.0E+00	BE795445.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2546	7511	12629	1.35	0.0E+00	BE283328.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2553	7518	12629	6.42	0.0E+00	BE792472.1	EST_HUMAN	601143722F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051389 5'
2555	7520	12637	1.06	0.0E+00	AB020710.1	NT	601594930F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939222 5'
2563	7527	12645	2.7	0.0E+00	4504686	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
2574	7537	12653	4	0.0E+00	AF173227.1	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2577	7540	12654	1.3	0.0E+00	AB011108.1	NT	Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2580	7543	12657	1.88	0.0E+00	AU133385.1	EST_HUMAN	Homo sapiens mRNA for KIAA0536 protein, partial cds
2581	7544	12658	1.75	0.0E+00	ME69225.1	NT	AU133385 NT2RP4 Homo sapiens cDNA clone NT2RP4001864 5'
2584	7547	12661	2.23	0.0E+00	AU130403.1	EST_HUMAN	Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds
2584	7547	12662	2.23	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2587	7550	12665	1.36	0.0E+00	AW887015.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2590	7553	12668	1.01	0.0E+00	BF000018.1	EST_HUMAN	RC1-OT0086-220300-011-d07 OT0086 Homo sapiens cDNA
2591	7554	12669	5.22	0.0E+00	BE383165.1	EST_HUMAN	7h15h05.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3316089 3'
2592	7555		8.33	0.0E+00	BE531283.1	EST_HUMAN	601298714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628923 5'
							601278373F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610267 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2616	7578	12680	1.38	0.0E+00	8922843	NT	Homo sapiens hypothetical protein FLJ11052 (FLJ11052), mRNA
2626	7586	12698	1.22	0.0E+00	AB037732.1	NT	Homo sapiens mRNA for KIAA1311 protein, partial cds
2650	7610		27.94	0.0E+00	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2651	7611	12721	1.31	0.0E+00	BE794894.1	EST_HUMAN	601589625F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943591 5'
2655	7615	12726	5.13	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
2656	7616	12727	5.03	0.0E+00	7659517	NT	Homo sapiens neuregulin 1 (NRG1), transcript variant SMDF, mRNA
2657	7617	12728	2.44	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL-1) gene, complete cds
2658	7618	12729	1.27	0.0E+00	AB051826.1	NT	Homo sapiens hG28K mRNA for GTP-binding protein like 1, complete cds
2684	7623	12735	26.29	0.0E+00	BE796376.1	EST_HUMAN	601591891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945983 5'
2665	7624	12736	1.5	0.0E+00	BF680632.1	EST_HUMAN	602155923F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297132 5'
2668	7778	12740	24.53	0.0E+00	BE568433.1	EST_HUMAN	601335485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689564 5'
2669	7627		2.28	0.0E+00	AV721647.1	EST_HUMAN	AV721647 HTB Homo sapiens cDNA clone HTBBYE09 5'
2671	7629	12743	2.82	0.0E+00	5174488	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2671	7629	12744	2.82	0.0E+00	5174488	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2672	7630	12745	1.27	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2672	7630	12746	1.27	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2673	7631	12747	2.26	0.0E+00	AF280185.1	NT	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2674	7632		51.51	0.0E+00	AV651086.1	EST_HUMAN	AV651086 GLC Homo sapiens cDNA clone GLCGLD07 3'
2675	7633	12748	3.33	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2675	7633	12749	3.33	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2682	7640	12756	19.56	0.0E+00	BE747193.1	EST_HUMAN	601580903F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929472 5'
2687	7645	12760	3.09	0.0E+00	BF037713.1	EST_HUMAN	601462038F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3885497 5'
2695	7653		0.93	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2696	7654	12768	2.53	0.0E+00	BF514110.1	EST_HUMAN	UI-H-BW1-armw-e-07-Q-UJ, s1 NCJ CGAP Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'
2703	7660		2.14	0.0E+00	4503088	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2708	7665	12776	1.05	0.0E+00	7705275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2708	7665	12777	1.05	0.0E+00	7705275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2709	7666	12778	2.88	0.0E+00	BF677694.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
2715	7672	12786	1.43	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2719	7676	12789	26.73	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2719	7676	12780	26.73	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2721	7678		11.75	0.0E+00	AB79163.1	EST_HUMAN	au55d04.Y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518663 5' similar to SW-R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2724	7681	12795	2.71	0.0E+00	BF530661.1	EST_HUMAN	602071957F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4214679 5'
2725	7682	12796	58.63	0.0E+00	BE872798.1	EST_HUMAN	601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854642 5'
2727	7684	12797	2.2	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2727	7684	12798	2.2	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2728	7685	12799	68.47	0.0E+00	BE300344.1	EST_HUMAN	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'
2728	7685	12800	68.47	0.0E+00	BE300344.1	EST_HUMAN	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'
2734	5251	10262	2.82	0.0E+00	S76830.1	NT	glycoprotein D-Duffy group antigen [human, blood, Genomic DNA, 3088 nt]
2737	7692		3.43	0.0E+00	AB033281.1	NT	Homo sapiens BTROP2 mRNA for F-box and WD-repeats protein isoform C, complete cds
2743	5747	10768	1.92	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2743	5747	10769	1.92	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2747	6032	11082	2.78	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2747	6032	11083	2.78	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2762	7783	12808	5.17	0.0E+00	X85980.1	NT	H.sapiens serine hydroxymethyltransferase pseudogene
2763	7784		1.34	0.0E+00	AF068624.1	NT	Homo sapiens 5-aminolevulinic synthase 2 (ALAS2) gene, complete cds
2765	7786		1.35	0.0E+00	AB040960.1	NT	Homo sapiens mRNA for KIAA1527 protein, partial cds
2771	7792		1.16	0.0E+00	AJ238852.1	NT	Homo sapiens partial rp13 gene for ribosomal protein L3, U82 snoRNA, U83a snoRNA and U83b snoRNA genes
2772	7793	12813	2.35	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2775	7796	12815	1.41	0.0E+00	M91803.1	NT	Human sodium channel mRNA
2777	7798	12817	1.6	0.0E+00	M80802.1	NT	Human AHNK nucleoprotein mRNA, 5' end
2781	7802		1.42	0.0E+00	X73428.1	NT	H.sapiens l33 gene for HLH type transcription factor
2783	7804		2.78	0.0E+00	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C063
2784	7805	12821	1.41	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2784	7805	12822	1.41	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2784	7805	12823	1.41	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2787	7808	12825	0.96	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
2792	7812	12828	36.19	0.0E+00	D90657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTG1P3) pseudogene
2792	7812	12830	36.19	0.0E+00	D90657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTG1P3) pseudogene
2795	7815	12833	4.89	0.0E+00	AL098657.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2798	7816		6.12	0.0E+00	Y10658.1	NT	H.sapiens mRNA for nuclear DNA helicase II
2797	7817		1.14	0.0E+00	AF152303.1	NT	Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2798	7818	12834	71.64	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA

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Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2788	7818	12835	71.84	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2810	7830	12846	2.53	0.0E+00	4507280	NT	Homo sapiens serine/threonine kinase 9 (STR9) mRNA
2813	7833	12850	1	0.0E+00	AL047599.1	EST_HUMAN	DKFZp586G0621_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586G0621
2814	7834		2.12	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (riatanome-associated) (CSPG4), mRNA
2817	7837	12852	5.88	0.0E+00	BE081898.1	EST_HUMAN	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA
2817	7837	12853	5.88	0.0E+00	BE081898.1	EST_HUMAN	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA
2822	7843	12861	0.85	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2822	7843	12862	0.85	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2825	7846	12868	3.1	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2825	7846	12867	3.1	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2826	7847	12868	1.03	0.0E+00	AA215579.1	EST_HUMAN	z96b11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683517 3' similar to contains Alu repetitive element;
2834	7854		4.09	0.0E+00	Y19210.1	NT	Homo sapiens hrb5 gene for hair keratin, exons 1 to 9
2836	7856	12875	1.08	0.0E+00	4758278	NT	Homo sapiens EphA4 (EPHA4) mRNA
2837	7857	12876	50.46	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2838	7858	12877	2.63	0.0E+00	AI561002.1	EST_HUMAN	tn18d07.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247
2838	7858	12878	2.63	0.0E+00	AI561002.1	EST_HUMAN	O16247 F44E7.2 PROTEIN. ;
2840	7860	12880	1.19	0.0E+00	P62740	SWISSPROT	tn18d07.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247
2841	7861	12881	1.05	0.0E+00	AF152338.1	NT	ZINC FINGER PROTEIN 132
2857	7877	12893	2.2	0.0E+00	AB033093.1	NT	Homo sapiens protocadherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2857	7877	12894	2.2	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2858	7878	12895	5.42	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2858	7878	12896	5.42	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2861	7881	12899	2.79	0.0E+00	7681903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2861	7881	12900	2.79	0.0E+00	7681903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2862	7882	12901	3.2	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q23) leukemia) (MLL-T4) mRNA
2862	7882	12902	3.2	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q23) leukemia) (MLL-T4) mRNA
2867	7886	12906	0.89	0.0E+00	BF110702.1	EST_HUMAN	7n40d03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1
							Q9VLN1 CG17293 PROTEIN. ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2867	7886	12907	0.99	0.0E+00	BF110702.1	EST_HUMAN	7n40403.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1
2875	7894	12917	2.17	0.0E+00	4505084	NT	Q9VLN1 CG17293 PROTEIN. ;
2875	7894	12918	2.17	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2882	7901	12923	1.65	0.0E+00	4758827	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2883	7902		1.14	0.0E+00	X88494.1	NT	Homo sapiens neurxin III (NRXN3) mRNA
2886	7905	12926	0.93	0.0E+00	AB033034.1	NT	H. sapiens mRNA for M phase phosphoprotein 10
2888	7907	12927	0.84	0.0E+00	X15309.1	NT	Homo sapiens mRNA for KIAA1208 protein, partial cds
2888	7907	12928	0.94	0.0E+00	X15309.1	NT	H. sapiens NF-H gene, exon 4
2890	7909	12930	8.37	0.0E+00	AF106275.1	NT	H. sapiens NF-H gene, exon 4
2904	7923		1.38	0.0E+00	A1149880.1	EST_HUMAN	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2912	7931	12950	1.21	0.0E+00	4506118	NT	q43f09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752809 3'
2913	7932	12951	4.29	0.0E+00	AB004884.1	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
2924	7943	12959	2.03	0.0E+00	7682273	NT	Homo sapiens mRNA for PKU-alpha, partial cds
2925	7944	12960	2.05	0.0E+00	5729755	NT	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA
2925	7944	12961	2.05	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2935	7954	12971	1.3	0.0E+00	AF114488.1	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2935	7954	12972	1.3	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
2958	7977	12982	1.23	0.0E+00	M74099.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
2967	7985	12989	0.84	0.0E+00	AW976266.1	EST_HUMAN	Human displacement protein (CCAAT) mRNA
2970	7988		4.06	0.0E+00	AF195953.1	NT	EST388375 MAGE resequences, MAGN Homo sapiens cDNA
2973	7991	13005	6.1	0.0E+00	5579469	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
2973	7991	13006	6.1	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
2975	7993		6.5	0.0E+00	AL359403.1	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
2978	7997	13010	1.96	0.0E+00	AF017433.1	NT	isoform 2 of a novel human mRNA from chromosome 22
							Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
							Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds, and L-type calcium channel alpha
2982	8000		1.97	0.0E+00	AF196779.1	NT	Human germline gene 16.1 for Ig lambda L-chain C region (IgL-C16.1)
3002	8020	13033	3.21	0.0E+00	X03529.1	NT	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds
3008	8025		1.81	0.0E+00	AF196355.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
3012	8029	13040	1.43	0.0E+00	AF094589.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3033	8050	13059	3.49	0.0E+00	AF285208.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3034	8051	13060	5.9	0.0E+00	AF148773.1	NT	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA
3036	8055	13063	3.23	0.0E+00	7682139	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3039	8056	13064	1.38	0.0E+00	AF042075.1	NT	Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds
3068	8084	13098	3.44	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3077	8093	13107	28.05	0.0E+00	L20941.1	NT	Human ferritin heavy chain mRNA, complete cds
3080	8096	13110	1.08	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3080	8096	13111	1.09	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3087	8103	13118	33.16	0.0E+00	T84870.1	EST_HUMAN	ye3203.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119453 3' similar to SP:S29539
3102	8118	13138	1.16	0.0E+00	BF243336.1	EST_HUMAN	S29539 BASIC PROTEIN, 23K - ;
3104	8120	13137	1.26	0.0E+00	A1868088.1	EST_HUMAN	601878507F1 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:4107433 5'
3109	8125	13144	4.08	0.0E+00	X98922.1	NT	wu12h10.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:2516803 3'
3109	8125	13145	4.08	0.0E+00	X98922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
3120	8136	13157	1.48	0.0E+00	4758827	NT	H.sapiens mRNA for gamma-glutamyltransferase
3120	8136	13158	1.48	0.0E+00	4758827	NT	Homo sapiens neurixin III (NRXN3) mRNA
3127	8143	13164	8.09	0.0E+00	4504658	NT	Homo sapiens neurixin III (NRXN3) mRNA
3145	8161	13182	12.78	0.0E+00	M28699.1	NT	Homo sapiens interlucin 1 receptor, type I (IL1R1) mRNA
3149	8165	13185	10.04	0.0E+00	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
3155	8171	13193	0.8	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3155	8171	13194	0.8	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3157	8173	13195	2.91	0.0E+00	AA774783.1	EST_HUMAN	ae87b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971133 3'
3165	8181	13203	5.5	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3165	8181	13204	5.5	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3175	8181	13212	1.57	0.0E+00	4557690	NT	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA
3180	8196	13219	0.98	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3187	8203	13225	1.97	0.0E+00	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes>
3180	8206	13228	3.59	0.0E+00	AF050584.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3193	8209	13230	1.14	0.0E+00	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
3193	8209	13231	1.14	0.0E+00	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
3201	10045	13238	2.89	0.0E+00	4502014	NT	Homo sapiens A kinase (PKA) anchor protein 1 (AKAP1), mRNA
3201	10045	13239	2.89	0.0E+00	4502014	NT	Homo sapiens A kinase (PKA) anchor protein 1 (AKAP1), mRNA
3218	8233	13254	2.91	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3219	8234	13255	1.97	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
3231	8246	13268	1.1	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3250	8263	13284	6	0.0E+00	AI589284.1	EST_HUMAN	tr58108.x2 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2222535 3' similar to SW:RL11_RAT
3257	8270	13292	2.09	0.0E+00	AF128893.1	NT	P25121 60S RIBOSOMAL PROTEIN L11, contains Alu repetitive element;
3257	8270	13293	2.09	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3258	8271	13294	0.78	0.0E+00	7657213	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3258	8271	13295	0.78	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3281	8274	13297	1.16	0.0E+00	4502582	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3281	8274	13298	1.16	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3284	8277	13300	11.21	0.0E+00	AF111163.1	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3266	8278	13302	1.25	0.0E+00	AB040940.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
3279	8281	13316	0.86	0.0E+00	AI632569.1	EST_HUMAN	Homo sapiens mRNA for KIAA1507 protein, partial cds
3312	8323	13346	3.08	0.0E+00	AU123684.1	EST_HUMAN	wb10104.x1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:2305279 3' similar to TR:Q91929 Q91929
3319	8329	13349	0.95	0.0E+00	7363436	NT	ZINC FINGER PROTEIN ;
3318	8329	13350	0.95	0.0E+00	7363436	NT	AU123684 NT2RM2 Homo sapiens cDNA clone N72RM2000735 5'
3322	8332	13352	1.91	0.0E+00	7708239	NT	Homo sapiens difactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3323	8333	13353	1.03	0.0E+00	AF211189.1	NT	Homo sapiens difactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3327	8337	13366	0.97	0.0E+00	AW867015.1	EST_HUMAN	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
3340	8349	13367	1.39	0.0E+00	7682401	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1a isoform (CACNA1I) mRNA, complete cds
3340	8349	13367	1.39	0.0E+00	7682401	NT	MR1-SN0033-100400-001-c08 SN0033 Homo sapiens cDNA
3341	8350	13368	1.13	0.0E+00	4502398	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3343	8352	13369	2.13	0.0E+00	5803067	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3352	7617	12728	1.45	0.0E+00	AF110763.1	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
3357	8365	13382	2.22	0.0E+00	7657038	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3358	8366	13383	1.37	0.0E+00	5453965	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3358	8366	13384	1.37	0.0E+00	5453965	NT	Homo sapiens death receptor 6 (DR6), mRNA
3361	8369	13388	0.96	0.0E+00	AJ272726.1	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
3361	8369	13389	0.96	0.0E+00	AJ272726.1	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
3362	8370	13390	4.76	0.0E+00	K02980.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
							Homo sapiens mRNA for rapa-2 (rapa gene)
							Homo sapiens mRNA for rapa-2 (rapa gene)
							Bacteriophage P1 replication region including repA, parA, and parB genes and IncA, IncB, and IncC
							Incompatibility determinants

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Table 4

Single Exon Probes Expressed in HBL100 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3364	8372	13392	1.12	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPR-T), mRNA
3367	8375	13395	1.1	0.0E+00	4557746	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
3373	8381	13400	4.09	0.0E+00	AI935159.1	EST_HUMAN	wp14d10.x1 NCJ CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634
3373	8381	13400	4.09	0.0E+00	AI935159.1	EST_HUMAN	NEURAL CELL ADHESION MOLECULE. ;
3377	8385	13406	1.61	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
3385	8393	13416	5.22	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3385	8393	13417	5.22	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3391	8399	13425	1.11	0.0E+00	M14123.1	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3397	8405	13431	6.63	0.0E+00	U43293.1	NT	Human MDS1A (AML1/MDS1 fusion) mRNA, partial cds
3401	8410	13435	0.99	0.0E+00	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3401	8410	13436	0.99	0.0E+00	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3405	8414	13441	2.65	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3405	8414	13442	2.65	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3413	8422	13451	1.04	0.0E+00	AF231922.1	NT	Homo sapiens chromosome 21 unknown mRNA
3423	8431	13457	1.44	0.0E+00	4508028	NT	Homo sapiens zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide) (ZNF45), mRNA
3426	8434	13459	2.04	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3428	8434	13460	2.04	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3428	8437	13463	1.11	0.0E+00	4826795	NT	Homo sapiens poliovirus voltage-gated channel, lck-related family, member 2 (KCNE2) mRNA
3431	8439	13466	1.05	0.0E+00	Q14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3436	8444	13470	0.83	0.0E+00	AJ384007.1	EST_HUMAN	ts35g12.x1 Soares_NihMPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:O00498
3439	8447	13473	1.05	0.0E+00	M10976.1	NT	O00498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN ;
3454	8462	13489	1.53	0.0E+00	AB032979.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
3454	8462	13490	1.53	0.0E+00	AB032979.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3463	8471	13498	0.86	0.0E+00	AV701869.1	EST_HUMAN	Homo sapiens mRNA for KIAA1153 protein, partial cds
3465	8473	13497	1.09	0.0E+00	4506884	NT	AV701869 ADB Homo sapiens cDNA clone ADBDA106 5'
3475	8475	13503	2.85	0.0E+00	AF078668.1	NT	Homo sapiens semenogelin II (SEMG2) mRNA
3475	8483	13503	1.11	0.0E+00	AL133204.1	NT	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds
3477	8485	13504	0.77	0.0E+00	AB040909.1	NT	Novel human gene mapping to chromosome X
3485	8493	13510	1.54	0.0E+00	8923087	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3493	8501	13515	0.94	0.0E+00	6897248	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
3493	8501	13515	0.94	0.0E+00	6897248	NT	Homo sapiens eal (Drosophila)-like 1 (SALL1), mRNA

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Single Exon Probes Expressed in HBL100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3493	8501	13516	0.94	0.0E+00	6997248	NT	Homo sapiens sal (<i>Drosophila</i>)-like 1 (SALL1), mRNA
3494	8502		1.7	0.0E+00	A1081907.1	EST_HUMAN	ox77c11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1662356 3' similar to WP:T1984.4
3496	8504	13519	1.01	0.0E+00	6325463	NT	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA
3500	8508		4.62	0.0E+00	AW852217.1	EST_HUMAN	QV0-CT0225-230300-169-e01 CT0225 Homo sapiens cDNA
3504	8512	13527	1.42	0.0E+00	4504294	NT	Homo sapiens H3 histone family, member K (H3FK), mRNA
3508	8516		5.83	0.0E+00	AF118846.1	NT	Homo sapiens gamma-glutamylcysteine synthetase (GLCLC) gene, partial cds
3509	8517	13528	7.79	0.0E+00	BF676393.1	EST_HUMAN	602084883F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4248596 5'
3513	8521		1.01	0.0E+00	AA888715.1	EST_HUMAN	oq94h06.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1594043 3' similar to contains MER28.b2
3522	8529	13539	1.4	0.0E+00	AW937977.1	EST_HUMAN	MER28 repetitive element;
3535	8541	13547	0.98	0.0E+00	BF672054.1	EST_HUMAN	QV0-DT0047-170200-123-g01 DT0047 Homo sapiens cDNA
3535	8541	13548	0.86	0.0E+00	BF672054.1	EST_HUMAN	602152486F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4283645 5'
3538	8542		1.13	0.0E+00	4826867	NT	602152486F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4283645 5'
3538	8544	13550	0.75	0.0E+00	AW664693.1	EST_HUMAN	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA
3538	8544	13551	0.75	0.0E+00	AW664693.1	EST_HUMAN	hi84g01.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2878024 3'
3541	8547	13555	0.72	0.0E+00	7662319	NT	hi84g01.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2878024 3'
3546	8553	13560	2.09	0.0E+00	4557752	NT	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
3546	8563	13561	2.09	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1), mRNA
3562	8569	13574	2.28	0.0E+00	D87327.1	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1), mRNA
3566	8573		14.47	0.0E+00	7669481	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
3563	8590	13594	3.35	0.0E+00	AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
3584	8591	13595	1.82	0.0E+00	AB007866.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
3586	8593	13596	4.2	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA; complete cds
3586	8593	13597	4.2	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA; complete cds
3592	8599	13605	1.04	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3592	8599	13606	1.04	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3595	8602	13608	1.83	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3595	8602	13609	1.83	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3596	8603	13610	0.93	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
3596	8603	13611	0.93	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
3599	8606	13614	1.43	0.0E+00	AW851714.1	EST_HUMAN	MR2-CT0222-281099-005-e05 CT0222 Homo sapiens cDNA

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Single Exon Probes Expressed in HBL100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3601	8608	13616	1.91	0.0E+00	5729928	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3603	8610	13618	1.09	0.0E+00	AB018339.1	NT	Homo sapiens mRNA for KIAA0796 protein, partial cds
3605	8612	13620	1	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3607	8614	13622	0.83	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3607	8614	13623	0.83	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3618	8625	13632	1.01	0.0E+00	5729733	NT	Homo sapiens activator of S phase kinase (ASK) mRNA
3618	8625	13633	1.01	0.0E+00	5729733	NT	Homo sapiens activator of S phase kinase (ASK) mRNA
3623	8630	13635	4.46	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-ajs-e-12-0-UI.st.NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3623	8630	13636	4.46	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-ajs-e-12-0-UI.st.NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3645	8651	13657	1.21	0.0E+00	AB004630.1	NT	Human gene for Type XIX collagen alpha1 chain, exon 6
3646	8652	13658	0.9	0.0E+00	AA463659.1	EST_HUMAN	aa08g01.1 Soares, NIH-MPU_S1 Homo sapiens cDNA clone IMAGE:812496 5' similar to SW:KRB4_SHEEP P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB4, [1];
3650	8656	13662	1.09	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3653	8659	13664	4.19	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3674	8679	13682	7.89	0.0E+00	7652183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3677	8682	13685	76.43	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
3683	8687	13689	1.39	0.0E+00	7657055	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3683	8687	13690	1.39	0.0E+00	7657055	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3729	8733	13731	0.98	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
3730	8734	13731	2.82	0.0E+00	AF178733.1	NT	Pan troglodytes olfactory receptor (PTR208) gene, partial cds
3733	8737	13735	2.36	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3733	8737	13736	2.36	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3734	8738	13737	1.15	0.0E+00	AF020091.1	NT	Homo sapiens smooth muscle myosin heavy chain SM1 mRNA, alternatively spliced, partial cds
3738	8742	13742	1.16	0.0E+00	4758011	NT	Homo sapiens RAB9, member RAS oncogene family (RAB9) mRNA
3741	8745	13745	1.16	0.0E+00	AF127851.1	NT	Gorilla olfactory receptor (GGO71) gene, partial cds
3741	8745	13746	1.16	0.0E+00	AF127851.1	NT	Gorilla olfactory receptor (GGO71) gene, partial cds
3742	8746	13747	1.18	0.0E+00	AI377668.1	EST_HUMAN	te62f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2091307 3'
3743	8747	13747	1.17	0.0E+00	AF162496.1	NT	Homo sapiens protocadherin beta 3 (PCDH-beta3) mRNA, complete cds
3744	8748	13748	1.26	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
3747	8751	13750	36.36	0.0E+00	S76865.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, complete cds
3749	8753	13752	2.74	0.0E+00	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA
3750	8754	13753	1.32	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3752	8756	13754	1.1	0.0E+00	AF069801.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds

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Single Exon Probes Expressed in HBL100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3752	8768	13755	1.1	0.0E+00	AF068601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3763	8767	13766	1.03	0.0E+00	4504534	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1D (HTR1D) mRNA
3769	8762	13762	0.81	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
3764	8767	13770	7.3	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3764	8767	13771	7.3	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3766	8769	13774	4.16	0.0E+00	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3767	8770	13775	1.26	0.0E+00	AF114488.1	NT	Homo sapiens interseitin short isoform (ITSN) mRNA, complete cds
3770	8773	13777	1.15	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3773	8776	13780	2.04	0.0E+00	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRP129), mRNA
3784	8787	13791	2.48	0.0E+00	A1864727.1	EST_HUMAN	wk01f01.x1 NCJ_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411065 3' similar to TR:O43340
3787	8780	13795	20.27	0.0E+00	4506742	NT	O43340 R28830_2: contains element PTR7 repetitive element;
3789	8792	13797	1.47	0.0E+00	AL040338.1	EST_HUMAN	Homo sapiens ribosomal protein S8 (RPS8), mRNA
3794	8797	13803	0.97	0.0E+00	6005887	NT	DKFZp434N0413_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0413 5'
3794	8797	13804	0.97	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3795	8798	13805	1.95	0.0E+00	4504138	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3796	8799	13805	1.87	0.0E+00	4505078	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
3800	8803	13808	0.87	0.0E+00	AF149412.1	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA
3808	8811	13817	1.69	0.0E+00	4506758	NT	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
3812	8815	13821	2.31	0.0E+00	4585642	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
3824	8826	13833	1.91	0.0E+00	AF129533.1	EST_HUMAN	Homo sapiens zinc finger protein (KIAA0412) mRNA
3826	8831	13838	3.61	0.0E+00	BE378602.1	EST_HUMAN	Homo sapiens F-box protein Fbl3b (FBL3B) mRNA, partial cds
3836	8838	13844	2.13	0.0E+00	AW580740.1	EST_HUMAN	601236966F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608800 5'
3837	8839	13845	1.01	0.0E+00	BE264998.1	EST_HUMAN	PM3-L10031-100100-003-h09 LT0031 Homo sapiens cDNA
3837	8839	13846	1.01	0.0E+00	BE264998.1	EST_HUMAN	601193827F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537774 5'
3868	8869	13872	4.2	0.0E+00	AF116195.1	NT	601193827F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537774 5'
3868	8869	13873	4.2	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3878	8879	13879	4.42	0.0E+00	M23910.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3881	8882	13882	5.99	0.0E+00	AL163303.2	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3887	8888	13887	0.93	0.0E+00	AL118494.1	NT	Human MHC class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2
3891	8891	13889	2.64	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C068
3899	8899	13897	2.2	0.0E+00	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
3911	8911	13911	113.41	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA

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Single Exon Probes Expressed in HBL100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3914	8914		1.34	0.0E+00	AI657076.1	EST_HUMAN	tt55g08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2244734 3' similar to TR:O60309 O60309
3916	8916	13910	2.58	0.0E+00	U09368.1	NT	KIAA0563 PROTEIN ;
3933	8932	13925	12.81	0.0E+00	AB015610.1	NT	Human zinc finger protein ZNF133
3941	8939		3.58	0.0E+00	AJ238617.1	NT	Chlorocephus aethiops mRNA for UGA suppressor tRNA-associated antigenic protein (RNA48 gene)
3951	8949	13938	1.39	0.0E+00	AB002314.2	NT	Homo sapiens mRNA for KIAA0316 protein, partial cds
3952	8950	13939	1.76	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
3953	8951	13940	2.58	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
3953	8951	13941	2.58	0.0E+00	AJ277276.1	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
3981	8959	13948	14.88	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
3981	8959	13948	14.88	0.0E+00	5032028	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,
3969	8968	13957	1.91	0.0E+00	4503914	NT	phosphoribosylaminimidazole synthetase (GART) mRNA
3973	8971	13959	4.78	0.0E+00	4885306	NT	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA
3974	8972	13960	1.41	0.0E+00	AB006625.1	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
3977	8976	13961	0.8	0.0E+00	4758807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
3978	8976	13962	7.12	0.0E+00	11419297	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA
3979	8977	13963	3.68	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
3980	8978		0.98	0.0E+00	AA018975.1	EST_HUMAN	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
3986	8984	13970	3.76	0.0E+00	AF165827.1	NT	ze55608.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:362920 5' similar to contains Alu repetitive element
3991	10050	13974	1.98	0.0E+00	AF157476.1	NT	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds
3995	6121	11150	1.11	0.0E+00	4826947	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
3995	6121	11151	1.11	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4000	8986	13984	1.04	0.0E+00	4503854	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4000	8996	13985	1.04	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4003	8999	13987	1.39	0.0E+00	8922391	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4003	8999	13988	1.39	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4006	9002	13989	1.03	0.0E+00	AB020702.1	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4012	9008	13997	6.13	0.0E+00	AI982597.1	EST_HUMAN	Homo sapiens mRNA for KIAA0895 protein, partial cds
4012	9008	13998	6.13	0.0E+00	AI982597.1	EST_HUMAN	wu04d04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2515975 3'
4014	9010	14000	2.24	0.0E+00	BE184856.1	EST_HUMAN	wu04d04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2515975 3'
4014	9010	14001	2.24	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4018	9014		10.6	0.0E+00	BE274217.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4024	9020	14007	1.02	0.0E+00	4507476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
4025	9021	14008	2.26	0.0E+00	5728725	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4032	9028		6.78	0.0E+00	AW675599.1	EST_HUMAN	ba51f04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800095 3' similar to SW:THI2_BOVIN
4037	9033	14021	0.95	0.0E+00	AW408788.1	EST_HUMAN	Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR ;
4039	9035	14024	1.51	0.0E+00	8922468	NT	UI-HF-BM0-adv-c-02-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063147 5'
4039	9035	14025	1.51	0.0E+00	8922468	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4048	9044		2.18	0.0E+00	5174632	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ), mRNA
4088	9082	14049	9.69	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element/contains element MER35 repetitive element ;
4088	9082	14050	9.69	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element/contains element MER35 repetitive element ;
4072	9086	14056	1.32	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
4085	9079	14068	0.94	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4085	9079	14069	0.94	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4087	9081	14072	1.45	0.0E+00	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
4101	9095	14079	1.28	0.0E+00	4758189	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4101	9095	14080	1.28	0.0E+00	4758189	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4109	9103		0.71	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4135	9130	14113	1.99	0.0E+00	AJ003145.1	NT	Homo sapiens mRNA for olfactory receptor protein, pseudogene
4151	9146	14130	2.21	0.0E+00	J02610.1	NT	Human apolipoprotein B-100 mRNA, complete cds
4164	9159	14146	0.86	0.0E+00	AW936689.1	EST_HUMAN	PM2-DT0023-080300-004-a08 DT0023 Homo sapiens cDNA
4171	9166	14153	4.94	0.0E+00	AF174590.1	NT	Homo sapiens F-box protein Fb14 (FBL4) mRNA, partial cds
4177	9171		3.4	0.0E+00	AI189844.1	EST_HUMAN	q223f08.x1 Soares_placenta_81c6weeks_2NbhP81c6W Homo sapiens cDNA clone IMAGE:1724579 3' similar to contains MER20.b2 MER20 repetitive element ;
4180	9173		5.07	0.0E+00	U14520.1	NT	Human CBFA3 (Osfar3) gene, partial cds
4183	9178	14180	0.82	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
4198	9181	14173	1.19	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4198	9181	14174	1.19	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4205	9188	14180	1.28	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4205	9188	14181	1.28	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4215	9208	14187	10.08	0.0E+00	6912281	NT	Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA
4235	9228		1.05	0.0E+00	AF153047.2	NT	Homo sapiens gap junction protein connexin-36 (CX36) gene, complete cds
4245	9239	14222	5.12	0.0E+00	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4249	9243	14227	4.71	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4249	9243	14228	4.71	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4250	9244	14229	1.5	0.0E+00	AW166933.1	EST_HUMAN	xc68e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2833514 3' similar to TR:P97365 P97365
4256	9250	14235	2.08	0.0E+00	X60483.1	NT	ZINC FINGER PROTEIN 64 ;
4256	9250	14238	2.08	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4261	9254	14242	11.18	0.0E+00	7662091	NT	H. sapiens KIAA0390 gene product (KIAA0390), mRNA
4261	9254	14243	11.18	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4274	9267	14258	11.95	0.0E+00	4885126	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4275	9268	14259	1.08	0.0E+00	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
4276	9269		0.99	0.0E+00	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4309	9301	14286	1.08	0.0E+00	7019456	NT	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA
4320	9312		6.33	0.0E+00	AF185953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
4325	9317	14289	2.98	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4325	9317	14300	2.98	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4330	9321	14306	0.81	0.0E+00	W26178.1	EST_HUMAN	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4330	9321	14307	0.81	0.0E+00	W26178.1	EST_HUMAN	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4344	9335		2.03	0.0E+00	AF200629.1	NT	Homo sapiens HPS1 gene, intron 5
4362	9353		0.78	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
4372	9364	14344	2.57	0.0E+00	AW084964.1	EST_HUMAN	xc68e08.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2588446 3' similar to SW-AHNK_HUMAN Q09666 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNK ;
4374	10032		1.15	0.0E+00	8051619	NT	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA
4375	9366	14346	0.91	0.0E+00	AF016050.1	NT	Homo sapiens vascular endothelial cell growth factor 165 receptor/neuropilin (VEGF165) mRNA, complete cds
4378	9369		7.59	0.0E+00	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4380	9371	14350	1.24	0.0E+00	AW381570.1	EST_HUMAN	PM1-HT0305-10T199-002-d03 HT0305 Homo sapiens cDNA
4386	9377	14357	1.16	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4386	9377	14358	1.16	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4388	9379	14360	1.24	0.0E+00	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4389	9380	14361	3.1	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNEH) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4398	9389	14372	1.05	0.0E+00	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ8/BIR1) gene, exon
4399	9390	14373	1.08	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4399	9390	14374	1.08	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4409	10053	14384	3.16	0.0E+00	6005973	NT	Homo sapiens zinc finger protein 195 (ZNF195), mRNA
4413	9403	14388	5.97	0.0E+00	AF208161.1	NT	Homo sapiens syncytin precursor, mRNA, complete cds
4418	9408	14395	1.83	0.0E+00	AF152337.1	NT	Homo sapiens protocadherin gamma C3 (PCDH-gamma-C3) mRNA, complete cds
4421	9411	14399	1.07	0.0E+00	5454175	NT	Homo sapiens zinc finger protein 211 (ZNF211), mRNA
4431	9421	14407	50.75	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4438	9428	14412	1.01	0.0E+00	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4442	9432	14415	1.5	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4446	9436	14420	1.11	0.0E+00	4502556	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA
4449	9439		1.16	0.0E+00	BE871908.1	EST_HUMAN	601447932F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852127 5'
4452	9442		2.72	0.0E+00	L35485.1	NT	Homo sapiens iduronate sulphate sulphatase (IDS) gene, complete cds
4454	9444	14423	11.71	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4454	9444	14424	11.71	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4471	9461	14440	2.89	0.0E+00	AF143314.1	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 5
4473	9463	14442	10.04	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4473	9463	14443	10.04	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4475	9465	14444	0.8	0.0E+00	AB018338.1	NT	Homo sapiens mRNA for KIAA0795 protein, partial cds
4490	9480		1.45	0.0E+00	AA174072.1	EST_HUMAN	zp18g08.s1 Stratagene fetal retina g37202 Homo sapiens cDNA clone IMAGE:608854 3'
4492	9482		1.39	0.0E+00	7657410	NT	Homo sapiens cdz (odd Oz/ten-m, Drosophila) homolog 1 (ODZ1), mRNA
4494	9484		2.8	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4495	9485	14463	1.18	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4496	9486	14464	5.1	0.0E+00	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4497	9487		1.83	0.0E+00	AB037521.1	NT	Homo sapiens gene for natriuretic protein, partial cds
4499	9489	14465	0.9	0.0E+00	AF185858.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
4502	9492	14469	1.33	0.0E+00	AB007866.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
4507	9497	14475	11.33	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4507	9497	14476	11.33	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4508	9498	14477	2.06	0.0E+00	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
4518	9508	14489	0.94	0.0E+00	L79810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4518	9508	14480	0.94	0.0E+00	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4518	9508	14491	0.94	0.0E+00	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4519	9509	14492	1.58	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4519	9509	14483	1.58	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4524	9514	14489	3.45	0.0E+00	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
4530	9520	14507	1.32	0.0E+00	BE080152.1	EST_HUMAN	QV2-BT0835-160400-142-05 BT0835 Homo sapiens cDNA IMAGE:767605 3'
4531	9521	14508	1.01	0.0E+00	AA418246.1	EST_HUMAN	z96b07.s1 Scarses_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:767605 3'
4536	9526		2.02	0.0E+00	AF086641.1	NT	Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region
4541	9530	14517	2.53	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4541	9530	14518	2.53	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4542	9531	14519	2.25	0.0E+00	M74099.1	NT	Human displacement protein (CCAAT) mRNA
4544	9533	14521	2.86	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4544	9533	14522	2.86	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4549	9537		1.17	0.0E+00	BE278730.1	EST_HUMAN	60115835F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505521 5'
4570	9558	14546	1.12	0.0E+00	5729817	NT	Homo sapiens ecotropic viral integration site 2B (EVI2B), mRNA
4570	9558	14547	1.12	0.0E+00	5729817	NT	Homo sapiens ecotropic viral integration site 2B (EVI2B), mRNA
4576	9563	14551	5.79	0.0E+00	M80902.1	NT	Human AHNK nucleoprotein mRNA, 5' end
4578	9566	14554	2.21	0.0E+00	M69197.1	NT	Human heptoglobin and heptoglobin-related protein (HP and HPR) genes, complete cds
4578	9566	14555	2.21	0.0E+00	M69197.1	NT	Human heptoglobin and heptoglobin-related protein (HP and HPR) genes, complete cds
4581	9569	14558	1.86	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4582	9570	14559	0.68	0.0E+00	7682478	NT	Homo sapiens KIAA1084 protein (KIAA1084), mRNA
4583	9571	14560	2.97	0.0E+00	7682181	NT	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA
4590	9578	14588	1.07	0.0E+00	U07563.1	NT	Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds
4594	9582	14572	1.24	0.0E+00	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4599	9587		1.15	0.0E+00	X58467.1	NT	Human CYP2D7AP pseudogene for cytochrome P450 2D6
4615	9600	14586	1.22	0.0E+00	AF026801.1	NT	Homo sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-26
4617	9602	14588	1.69	0.0E+00	6877700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4617	9602	14589	1.69	0.0E+00	6877700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4618	9603	14590	0.75	0.0E+00	7018320	NT	Homo sapiens proteinx0008 (ADO13), mRNA
4618	9603	14591	0.75	0.0E+00	7018320	NT	Homo sapiens proteinx0008 (ADO13), mRNA
4641	9626	14618	1.65	0.0E+00	AW44637.1	EST_HUMAN	U1-H-B13-ajw-c-04-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'
4647	9632	14627	1.01	0.0E+00	AF303134.1	NT	Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds

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4649	9834		1.44	0.0E+00	AF083242.1	NT	Homo sapiens HSPC024-iso mRNA, complete cds
4688	9873	14655	0.68	0.0E+00	J00191.1	NT	Human MHC class I transplantation antigen (hla) gene
4688	9873	14656	0.68	0.0E+00	J00191.1	NT	Human MHC class I transplantation antigen (hla) gene
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4694	9679		6.96	0.0E+00	AF240786.1	NT	M.fascicularis mRNA for metalloprotease-like, disintegrin-like protein, IVa
4698	9683	14668	2.39	0.0E+00	X87205.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSOR9) mRNA, complete cds
4700	9685	14668	1.77	0.0E+00	AF084478.1	NT	Mus musculus zinc finger transcription factor Kaiso mRNA, complete cds
4701	9686	14669	1.47	0.0E+00	AF097416.1	NT	Mus musculus zinc finger transcription factor Kaiso mRNA, complete cds
4702	9687	14670	4.25	0.0E+00	4503766	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4704	9689	14672	13.59	0.0E+00	4895048	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA
4706	9691	14674	2.35	0.0E+00	8922180	NT	Homo sapiens hypothetical protein DKFZp762E1312 (DKFZp762E1312), mRNA
4709	9694	14678	7.7	0.0E+00	8923080	NT	Homo sapiens hypothetical protein FLJ20073 (FLJ20073), mRNA
4712	9697	14681	2.67	0.0E+00	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4713	9698	14682	1.91	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1- J61 segments; and Tcr-C-alpha gene, exons 1-4
4713	9698	14683	1.91	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1- J61 segments; and Tcr-C-alpha gene, exons 1-4
4715	9700	14685	1.8	0.0E+00	X94628.1	NT	H. sapiens MeCP-2 gene
4715	9700	14686	1.8	0.0E+00	X94628.1	NT	H. sapiens MeCP-2 gene
4718	9703	14689	1.97	0.0E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
							Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 28kD (TAF21) mRNA
4727	9712	14697	1.27	0.0E+00	5032150	NT	H. sapiens MICA gene
4732	9717	14702	3.82	0.0E+00	X92841.1	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
4734	9719	14704	1.68	0.0E+00	4585642	NT	Homo sapiens mRNA for KIAA1443 protein, partial cds
4735	9720	14705	1.08	0.0E+00	AB037894.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
4736	9721	14706	0.92	0.0E+00	AB014533.1	NT	Mus musculus zinc finger protein interacting with K protein 1 (Zfk1), mRNA
4737	9722	14707	2.29	0.0E+00	6677648	NT	Homo sapiens meningoangioma expressed antigen 6 (colloid-coil proline-rich) (MGEA6), mRNA
4738	9723	14708	1.04	0.0E+00	5174560	NT	Homo sapiens desmoplakin (DPI, DPL1) (DSP) mRNA
4740	9725	14710	1.45	0.0E+00	4758189	NT	Homo sapiens MHC class 1 region
4744	9729	14716	38.01	0.0E+00	AF055056.1	NT	Homo sapiens opicid receptor, delta 1 (OPRD1) mRNA
4746	9731		2.39	0.0E+00	4505508	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds
4747	9732	14719	2.63	0.0E+00	AF091711.1	NT	Homo sapiens COL4A8 gene for alpha(IV) collagen, exon 44 and partial cds
4760	9744	14730	1.02	0.0E+00	D83562.1	NT	

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Table 4
Single Exon Probes Expressed in HBL100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4762	9746	14732	1.96	0.0E+00	4503684	NT	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDPs) mRNA
4764	9748	14735	1.13	0.0E+00	A1249082.1	EST_HUMAN	qh68d08.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849839 3' similar to SW:ATPN_BOVIN Q28852 ATP SYNTHASE G CHAIN, MITOCHONDRIAL ;
4764	9748	14736	1.13	0.0E+00	A1249082.1	EST_HUMAN	qh68d08.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849839 3' similar to SW:ATPN_BOVIN Q28852 ATP SYNTHASE G CHAIN, MITOCHONDRIAL ;
4768	9752		1.07	0.0E+00	A1291129.1	EST_HUMAN	qm15f05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881921 3' similar to TR:Q61632 Q61632 EN-2/LACZ FUSION PROTEIN ;
4795	9779	14762	1.2	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4801	9785	14767	1.02	0.0E+00	7662319	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
4808	9792	14774	0.86	0.0E+00	AA205437.1	EST_HUMAN	zq68d06.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:646547 3'
4813	9797	14781	6.67	0.0E+00	U14987.1	NT	Human ribosomal protein L21 mRNA, complete cds
4823	9807	14789	1.6	0.0E+00	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
4825	9809		2.99	0.0E+00	BE408863.1	EST_HUMAN	601303729F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:36381 18 5'
4829	9813	14794	3.55	0.0E+00	4758193	NT	Homo sapiens desmoplakin (DPI, DPLI) (DSP) mRNA
4836	9820	14797	2.16	0.0E+00	AB028966.1	NT	Homo sapiens mRNA for KIAA1043 protein, partial cds
4848	9830	14804	2.53	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
4848	9830	14805	2.53	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
4862	9843	14815	1	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN ;
4862	9843	14816	1	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN ;
4862	9843	14817	1	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN ;
4864	9844	14818	1.59	0.0E+00	AF161463.1	NT	Homo sapiens HSPC114 mRNA, complete cds
4864	9844	14819	1.59	0.0E+00	AF161463.1	NT	Homo sapiens HSPC114 mRNA, complete cds
4867	5275	10289	0.81	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
4870	9849		0.92	0.0E+00	4758225	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
4881	9860	14831	1.28	0.0E+00	AF016705.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 3
4883	9862	14833	1.27	0.0E+00	U53588.1	NT	Homo sapiens MHC class 1 region
4887	9866		1.11	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4890	9869		27.33	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
4913	9892	14866	3.61	0.0E+00	X62988.1	NT	Bacillus amyloquelicifaciens sacB gene for levansucrase (EC 2.4.1.10)
4927	9904	14882	2.48	0.0E+00	AF272663.1	NT	Homo sapiens gephyrin mRNA, complete cds

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Table 4
Single Exon Probes Expressed in HBL100

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4930	9907	14884	1.13	0.0E+00	5454153	NT	Homo sapiens cyclophilin (USA-CYP) mRNA
4936	9913	14891	0.99	0.0E+00	AA683268.1	EST_HUMAN	aa92b04.s1 Striatagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1020387 3'
4951	9928	14906	0.95	0.0E+00	4557362	NT	Homo sapiens PR domain containing 1, with ZNF domain (PRDM1) mRNA
4957	9934	14912	0.72	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
4965	9942	14919	0.92	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
4980	9955	14933	0.92	0.0E+00	7662421	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
4981	9956	14934	0.67	0.0E+00	4826795	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA
4990	9963	14940	1.07	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
4990	9963	14941	1.07	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
5009	9980	14955	1.27	0.0E+00	7657203	NT	Homo sapiens acidic 82 kDa protein mRNA (HSU15562), mRNA
5034	10005	14976	1.17	0.0E+00	4758021	NT	Homo sapiens coagulation factor C (Limulus polyphemus) homology (COCH), mRNA
5049	10020	14989	0.99	0.0E+00	6877700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
5049	10020	14990	0.99	0.0E+00	6877700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
5053	10024	14993	0.74	0.0E+00	7657336	NT	Homo sapiens mult. (E. coli) homolog 3 (MLH3), mRNA
5068	10037	15004	0.75	0.0E+00	AL044081.1	EST_HUMAN	DKFZp434L2428_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2428 5'

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human Breast comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 5,074 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 5,075 - 10,058.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Breast comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 5,074 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human Breast.

35

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 5,075 - 10,058 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Breast which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of
10 SEQ ID NOS.: 10,059 - 15,009, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human Breast.

16. A single exon nucleic acid probe as claimed in any one
15 of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

17. A single exon nucleic acid probe as claimed in any one
20 of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

25

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

30 20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

21. A single exon nucleic acid probe as claimed in any one
35 of claims 13 - 20, wherein said probe lacks homopolymeric

stretches of A or T.

22. A method of measuring gene expression in a sample derived from human Breast, comprising:

5 contacting the microarray of claim 12, with a first
 collection of detectably labeled nucleic acids,
 said first collection of nucleic acids derived
 from mRNA of human Breast; and then
 measuring the label detectably bound to each probe of
10 said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

15 algorithmically predicting at least one exon from
 genomic sequence of said eukaryote; and then
 detecting specific hybridization of detectably labeled
 nucleic acids to a single exon probe,
 wherein said detectably labeled nucleic acids are derived
 from mRNA from the Breast of said eukaryote, said probe is
20 a single exon probe having a fragment identical in sequence
 to, or complementary in sequence to, said predicted exon,
 said probe is included within a microarray according to
 claim 12, and said fragment is selectively hybridizable at
 high stringency.

25

24. A method of assigning exons to a single gene, comprising:

 identifying a plurality of exons from genomic
 sequence according to the method of claim 23; and
30 then
 measuring the expression of each of said exons in a
 plurality of tissues and/or cell types using
 hybridization to single exon microarrays having a
 probe with said exon,
35 wherein a common pattern of expression of said exons in

said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

25. A nucleic acid sequence as set out in any of SEQ ID
5 NOS: 1 - 10,058 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of
SEQ ID Nos: 1 - 10,058.

10 27. A peptide comprising a sequence as set out in any of
SEQ ID Nos: 10,059 - 15,009.

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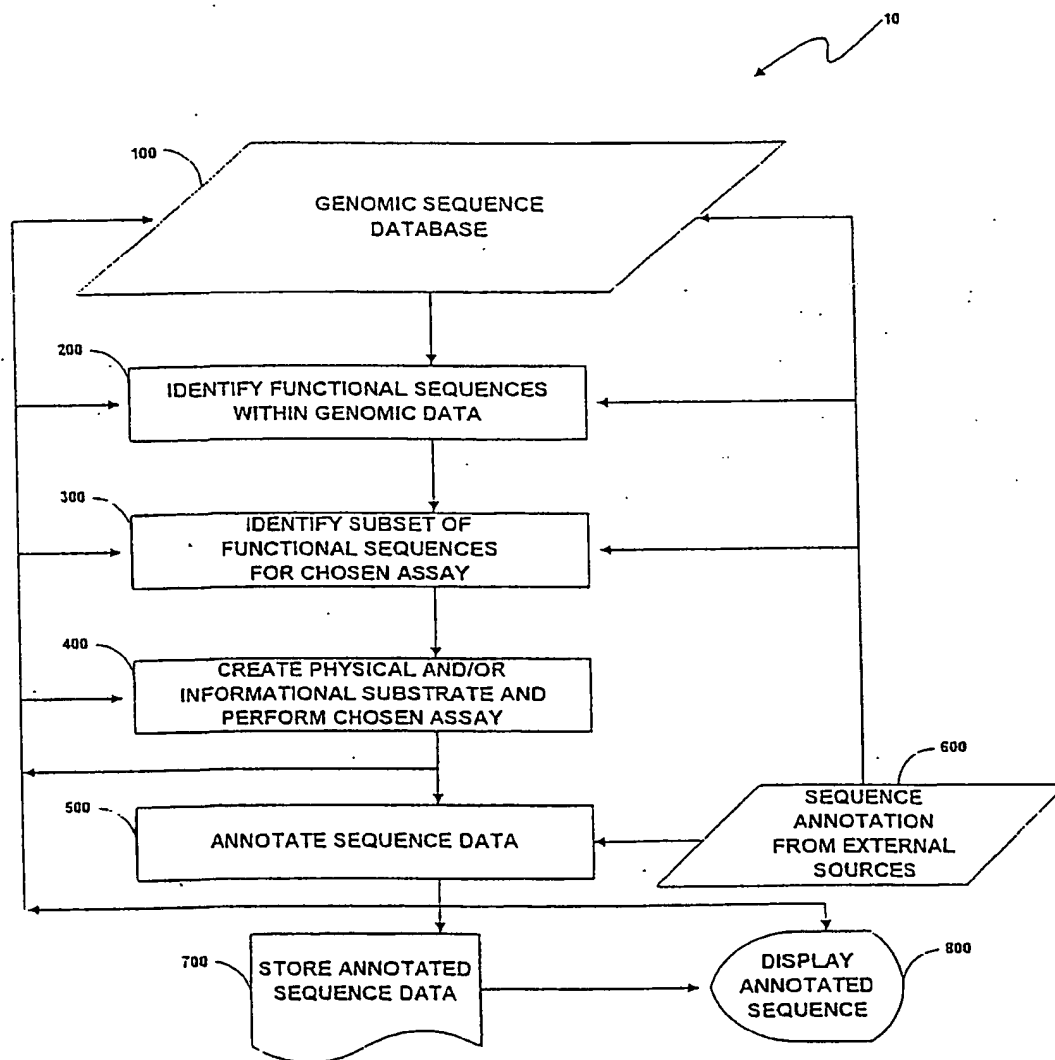


Fig. 1

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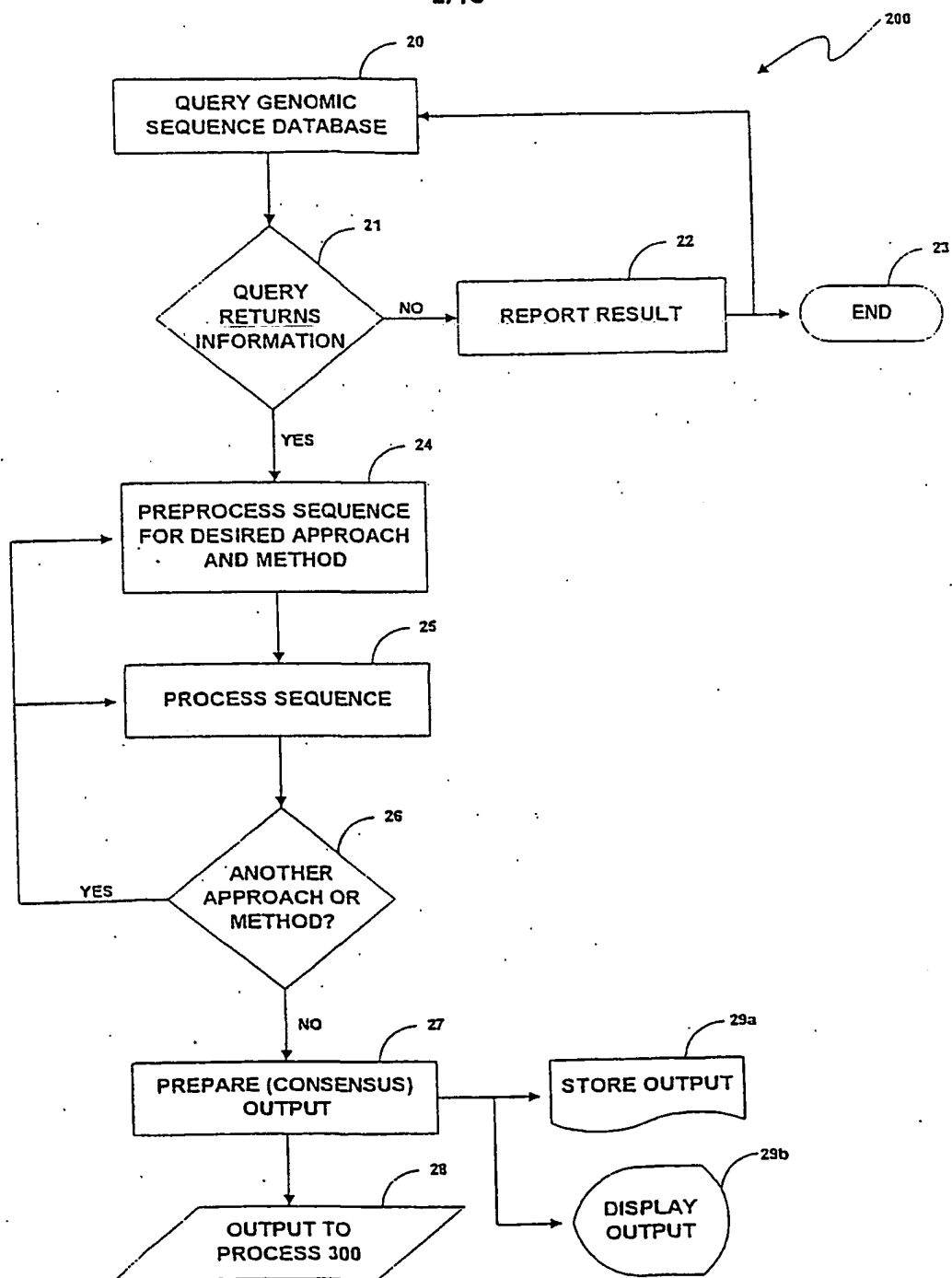


Fig. 2

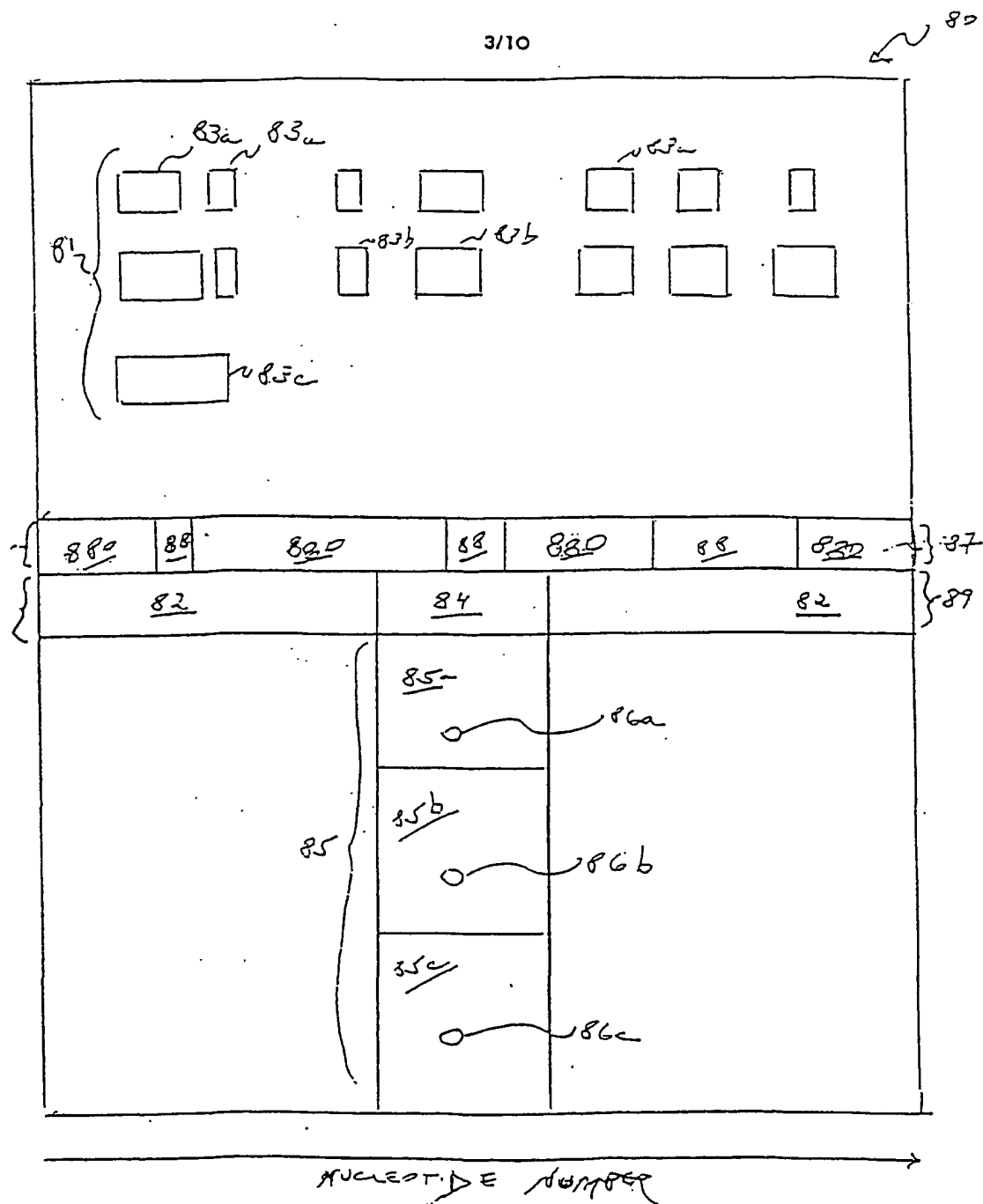


Fig. 3

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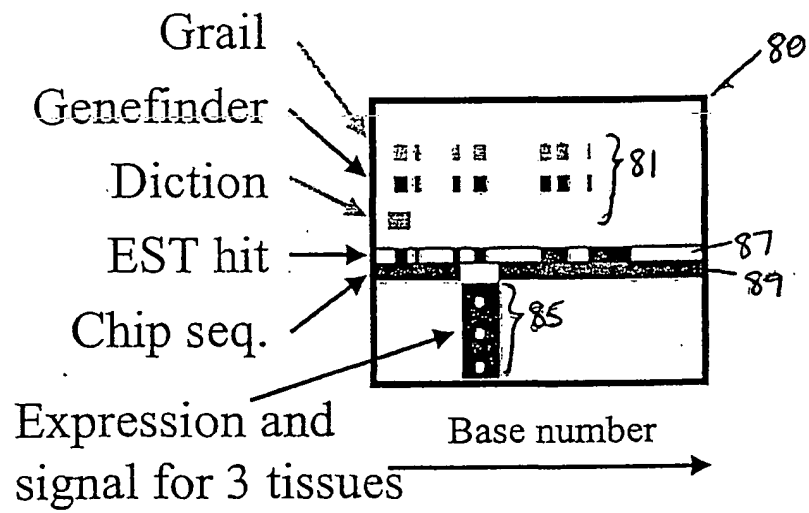


Fig. 4

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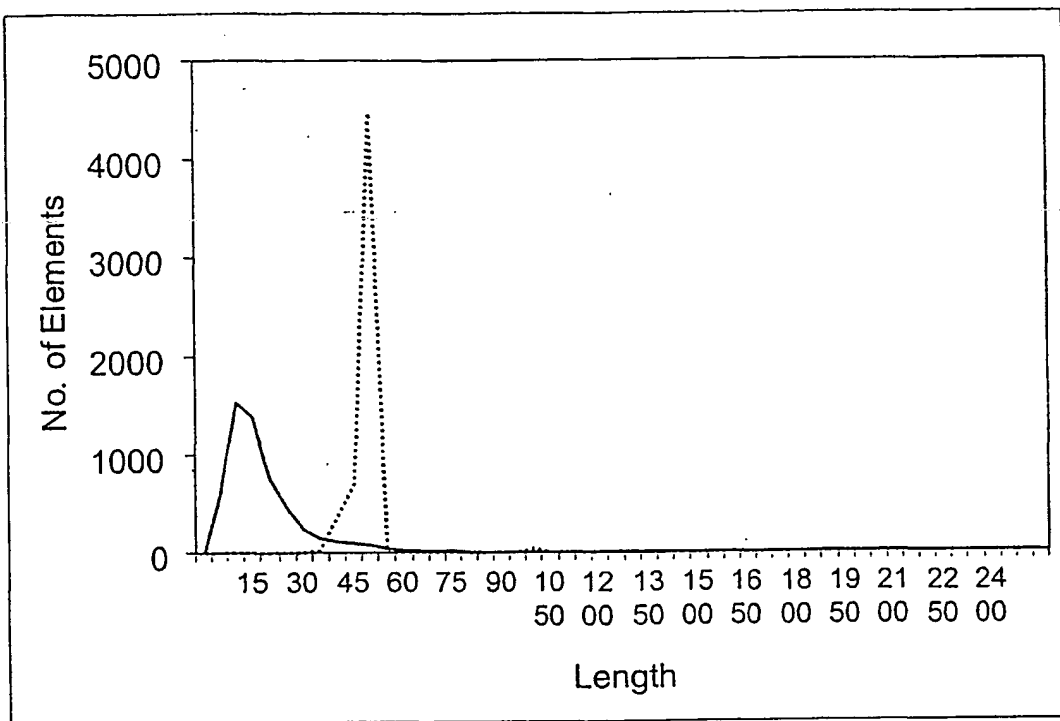


Fig. 5

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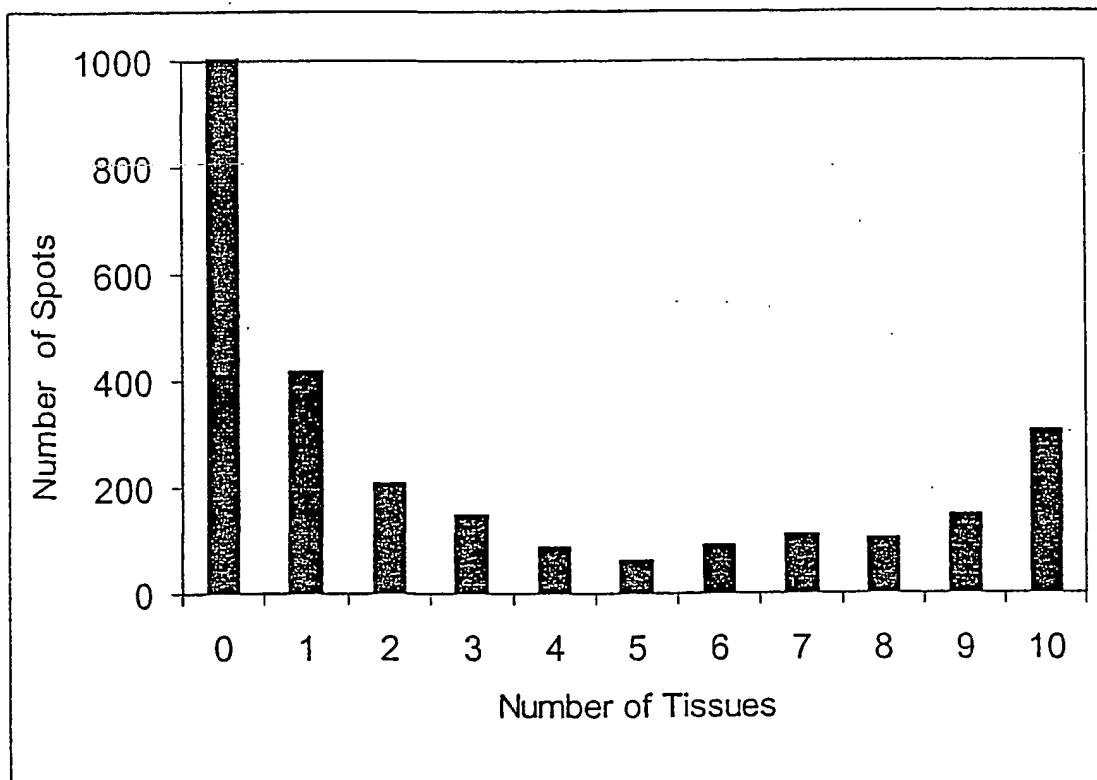


Fig. 6

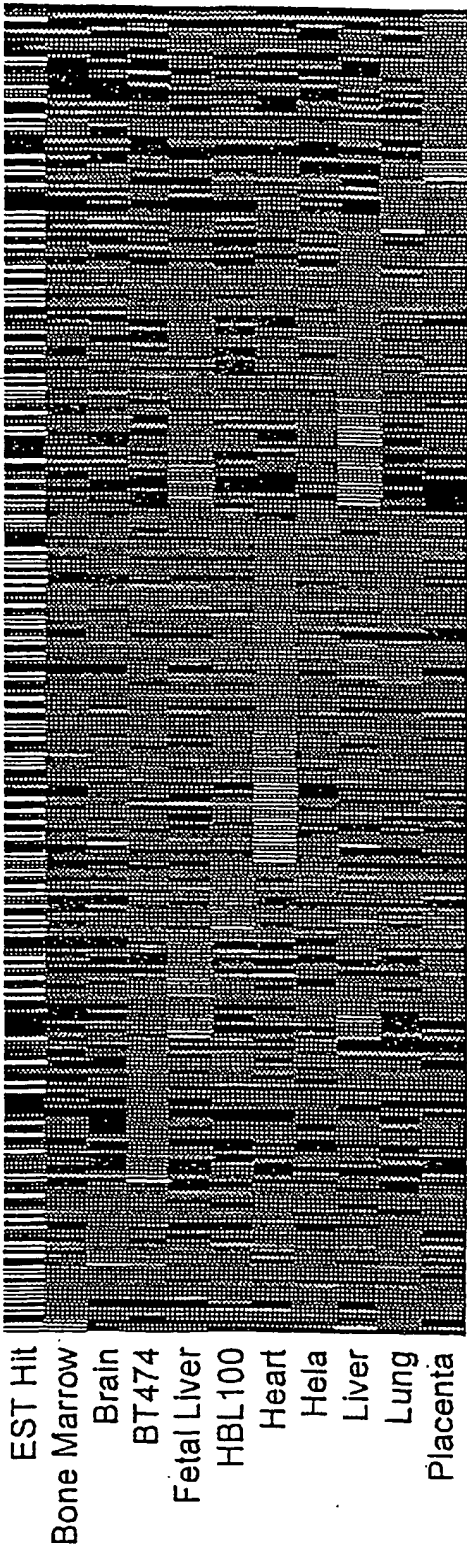


Fig. 7a

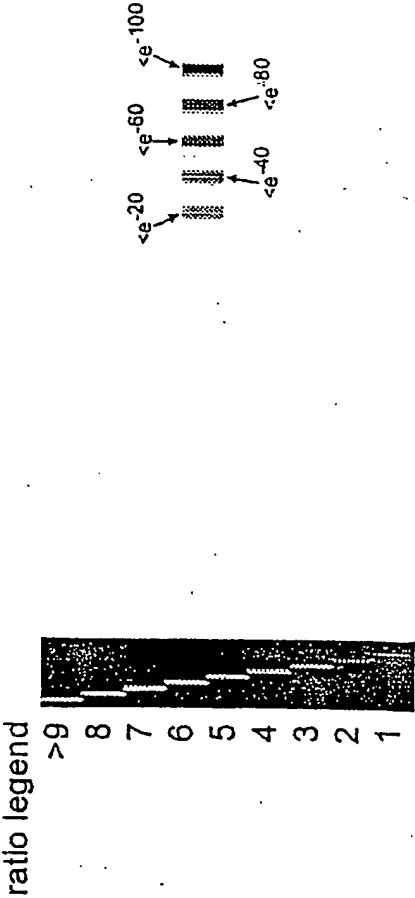


Fig. 7c

Fig. 7b

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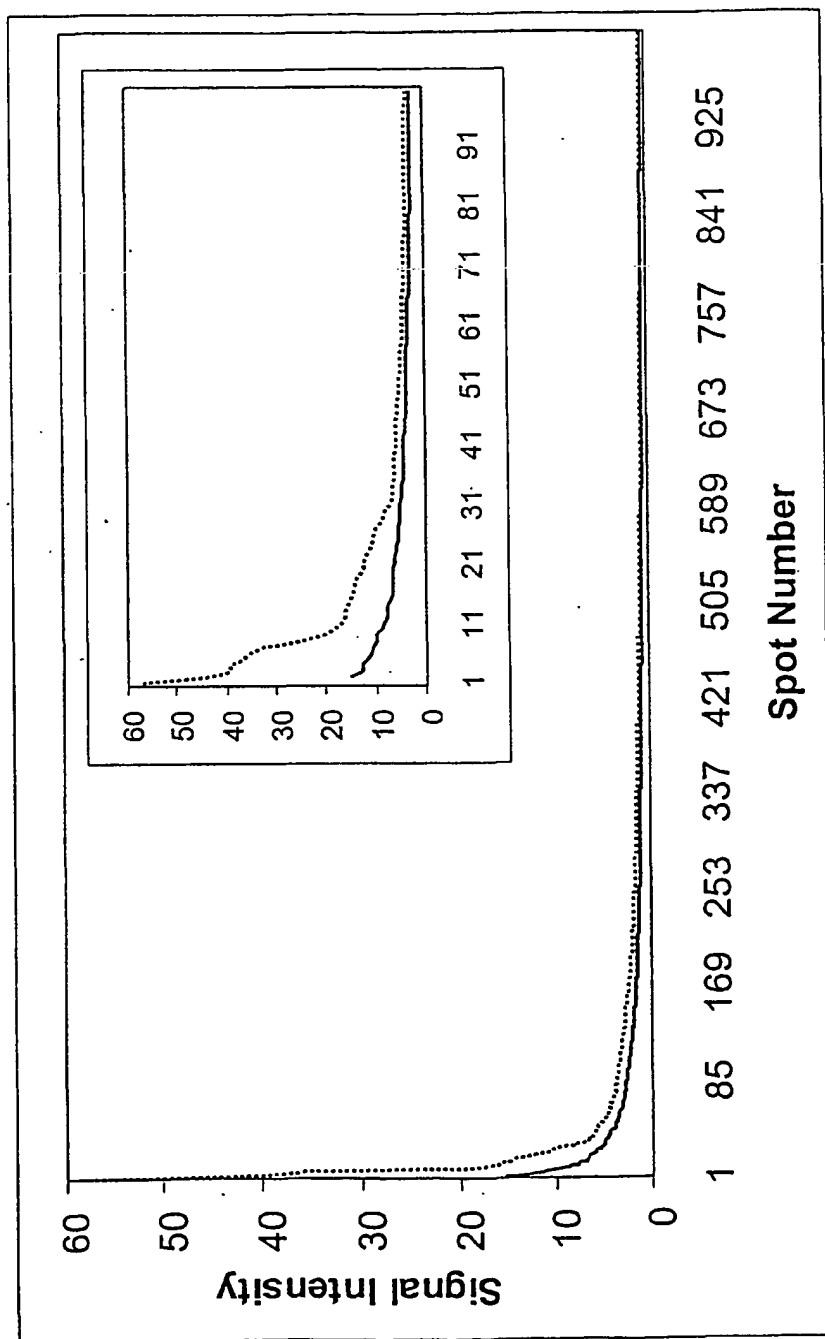


Fig. 8

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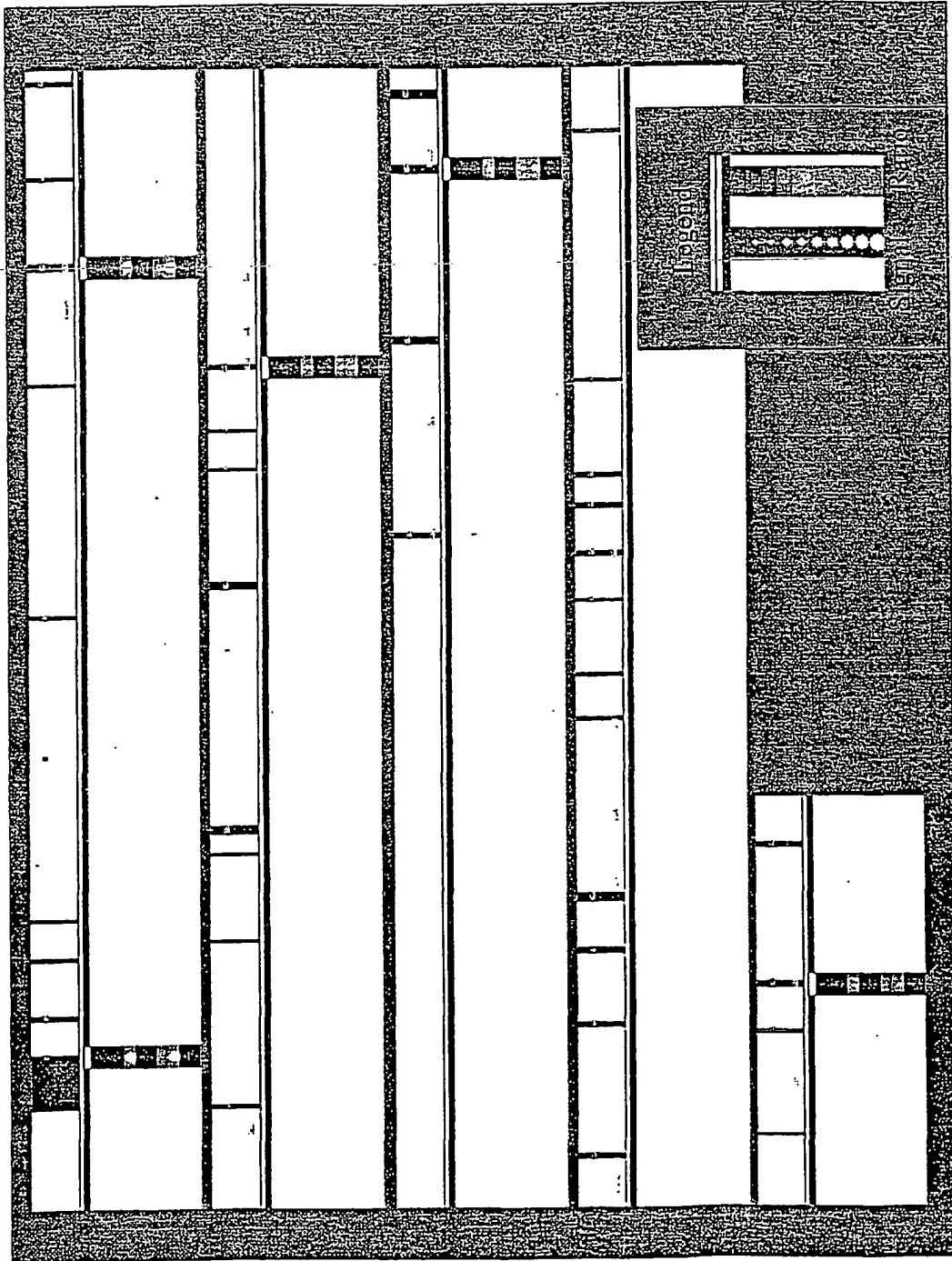
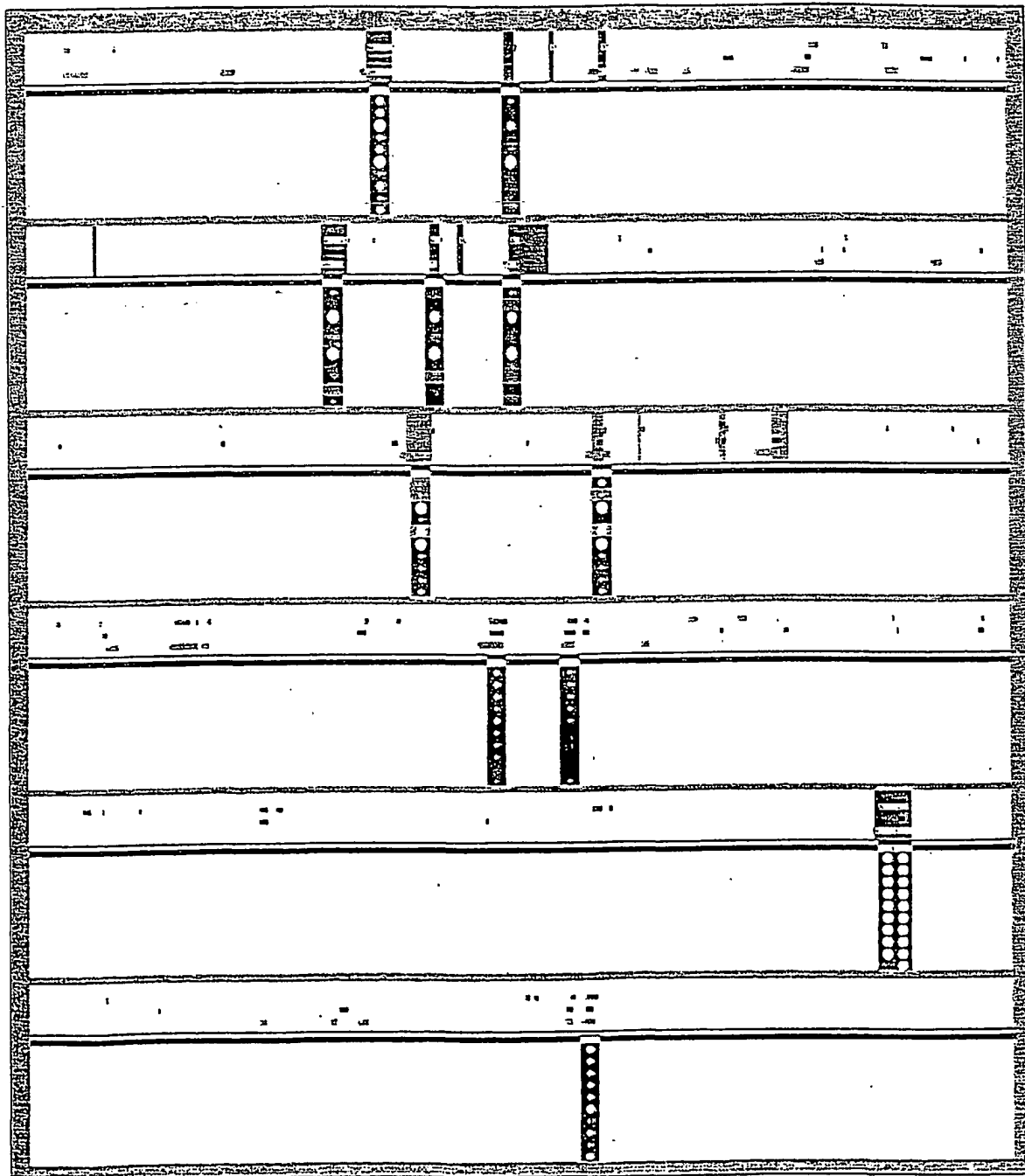


Fig. 9

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Fig. 10



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- (75) Inventors/Applicants (*for US only*): PENN, Sharron, G. [GB/US]; 617 South Delaware Street, San Mateo, CA 94402 (US). HANZEL, David, K. [US/US]; 988 Loma Verde Avenue, Palo Alto, CA 94303 (US). CHEN, Wen-sheng [CN/US]; 210 Easy Street #25, Mountain View, CA 94043 (US). RANK, David, R. [US/US]; 117 El Dorado Commons, Fremont, CA 94539 (US).
- (74) Agent: RONNING, Royal, N., Jr.; Amersham Pharmacia Biotech, Inc., 800 Centennial Avenue, Piscataway, NJ 08855 (US).
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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BREAST AND HBL 100 CELLS

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human HBL 100 cells is described. Also described are single exon nucleic acid probes expressed in the HBL 100 cells and their use in methods for detecting gene expression.



WO 01/057270 A3

INTERNATIONAL SEARCH REPORT

Int. Application No.

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A. CLASSIFICATION OF SUBJECT MATTER

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According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12Q C07K G06F

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, WPI Data, EPO-Internal, MEDLINE, EMBASE, CHEM ABS Data, SEQUENCE SEARCH

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	STAUDER R ET AL: "Different CD44 splicing patterns define prognostic subgroups in multiple myeloma." BLOOD, (1996). VOL. 88, NO. 8, PP. 3101-8. JOURNAL CODE: A86. ISSN: 0006-4971., XP001033913 Basel Institute for Immunology, Switzerland. the whole document	13
X	WO 99 15701 A (ONCORMED INC ;LESCALLET JENNIFER L (US); THURBER DENISE B (US)) 1 April 1999 (1999-04-01) page 2, line 31 -page 3, line 33; claims -/--	1-27

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Date of the actual completion of the international search

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INTERNATIONAL SEARCH REPORT

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 99 39004 A (COLLINS FRANCIS S ;CHEE MARK (US); EDGEMON KEITH (US); US HEALTH () 5 August 1999 (1999-08-05) page 20, line 20 -page 25, line 20 ----	1-21
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In International Application No

PCT/US 01/00661

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

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X	DATABASE EBI 'Online! 9 May 1997 (1997-05-09) MARRA M. ET AL.: "The WashU-HHMI mouse EST project; vc72c02.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE: 780098" Database accession no. AA414703 XP002208274 abstract -----	13,14, 18,20,21
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INTERNATIONAL SEARCH REPORT

national application No.
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Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
1-27 (partially)
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-27 (partially)

A probe comprising the nucleotide sequence SEQ ID 1 (see claim 13), or a fragment thereof having a length of at least 15 bp (see ISA form 206), in particular comprising the sequence SEQ ID 5075 (see p. 92 of the description, which indicates that this sequence corresponds to the exon comprised in SEQ ID 1), spatially addressable set of probes comprising the said sequence (claim 1), microarrays comprising said sequence (claim 12), a method for measuring gene expression (claim 22), a method for identifying exons (claim 23) and a method for assigning exons to a single gene (claim 24) comprising using the said arrays, the peptide encoded by SEQ ID 1 or 5075 (claims 26-27) having the sequence SEQ ID 10059 (see ISA form 206), which is the translation from SEQ ID 5075 (see p. 74 of the description).

2. Claims: 1-27 (partially)

A probe comprising the nucleotide sequence SEQ ID 2, or a fragment thereof having a length of at least 15 bp (see ISA form 206), in particular comprising the sequence SEQ ID 5076 (see p. 92 of the description, which indicates that this sequence corresponds to the exon comprised in SEQ ID 2), spatially addressable arrays comprising the said sequence, a method for measuring gene expression, a method for identifying exons and a method for assigning exons to a single gene comprising using the said arrays, a peptide encoded by SEQ ID 2 or 13116 having the sequence SEQ ID 10060, which is the translation from SEQ ID 5076 (see p. 74 of the description) (see however last paragraph of the reasoning hereinafter).

...Inventions 3-5074: similar subject-matter as above related to SEQ IDs 3-5074.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

The following statements concerning the impossibility of performing a meaningful search according to Art. 17(2) PCT are made for the subject-matter for which a search has been performed and which has been identified as inventions 1 and 2.

1) Claims 1-3, 5, 6, 8-15 and 18-24 relate to fragments of undisclosed length or characteristics which cannot therefore be meaningfully searched. These claims have thus been searched only insofar as related to fragments having a length of at least 15 nt (see claim 15 and description pages 10, l. 10-17 and 69, l. 14-26).

2) Present claims 1-12 and 22-24 relate to an extremely large number of possible sets of nucleic acid probes comprising SEQ ID 1 and 2 and microarrays comprising the said sets. Therefore, the claims lack clarity and conciseness (Art. 6 PCT) to such an extent as to render a meaningful search over their whole scope impossible. Consequently, with respect to the said sets and microarrays the search has been carried out only insofar as related to the SEQ ID 1 and 2 as such.

3) In view of the absence of any indication as to which other peptides could be encoded by SEQ ID 1 and 2, the search with respect to claim 26 has been limited to the peptide sequences actually disclosed in the application, i.e. 10059 and 10060 (Art. 6 PCT).

4) Claims 15-21 relate to nucleic acid probes, solely defined in that they code for a polypeptide having the sequence SEQ ID 10059 or 10060. However, a peptide is potentially coded by an extremely large number of nucleic acid sequences. Hence, claims 15-21 lack clarity and conciseness to such an extent as to render a meaningful search over their whole scope impossible. The search has thus been limited to SEQ ID 1, 2, 5075 and 5076.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 01/00661

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